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GenCore version 5.1.6
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                  Copyright
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- protein search, using sw model OM protein

September Run on:

5, 2004, 09:47:29; Search time 6.90909 Seconds (without alignments) 125.302 Million cell updates/sec

US-09-761-636A-10 50 1 CSVPLTSVC 9 score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283366 segs, 96191526 residues Searched:

283366 Total number of hits satisfying chosen parameters:

length: 0 length: 2000000000 Minimum DB Maximum DB

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR 78:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

pir4:*

	Description	(c) k_openi [Odnacha	probable membrane	hypotherical prote	hypothetical 38.5k		۲	uvrC protein - Pse	=	hypotherical prote	transcription requi	napin - Swedish tu	-	ירה אונים אויי	3	Sin's	Sin	allergen Sin a T	١.	nanin BG9 nrecurso	napin 2 predirect	m	or.	2S storage protein	Storage		in (clon	mgii (clones Buwi	monophenol monoper	major allergen lar
SEIN		 																												
SUMMARIES	ID	S48719	AD0990	CB6015	S47693	C91169	F64484	B55538	S54788	T29764	D97130	A37931	S65447	NWRP1	865478	S65481	565482	S65480	T34649	PS0426	NWRP2	S07828	A25997	S25137	S25130	S25134	S10018	S52025	YRNC	835592
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	Query Match Length	1487	349	364	376	376	432	22	591	2180	91	124	127	133	145	145	145	145	152	155	178	178	178	178	178	178	180	180	621	92
ф	Query	86.0	82.0	82.0	82.0	82.0	78.0	76.0	72.0	72.0	70.0	70.0	70.0	70.0	70.0	70.0	70.0	70.0	70.0	70.0	70.0	70.0	70.0	70.0	70.0	70.0	70.0	70.0	70.0	68.0
	Score	43	41	41	41	41	39	38	36	36	35	35	35	35	35	35	35	32	35	35	35	35	35	35	35	35	35	35	35	34
	Result No.	Н	7	m	4	2	9	7	c o	ov.	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29

dehydro	hypothetical prote	NADH2 dehydrogenas	NADH2 dehydrogenas	NADH2 dehydrogenas	NADH2 dehydrogenas	NADH2 dehydrogenae	hypothetical trans	e proposa se	prostacyclin recen	proline/betaine tr	hypotherical profe	arginine - tRNA liga	ardinine-tana	hypothetical prote
T12116	B96583	T11729	T11687	T11702	T11697	T11731	S70841	S77634	A57066	E71716	T08794	JC4365	JN0870	T17122
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68.0	68.0	68.0	68.0	68.0	68.0	68.0	68.0	68.0	68.0	68.0	68.0	68.0	68.0	0.89
34	34	34	34	34	34	34	34	34	34	34	34	34	34	34
30	32	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

S48719
Shopholipase-A(2) receptor protein - mouse
C;Species: Mus musculus (house mouse)
C;Date: 07-May-1995 #sequence_revision 21-Jul-1995 #text_change 20-Jun-2000
C;Date: 07-May-1995 #sequence_revision 21-Jul-1995 #text_change 20-Jun-2000
C;Accession: \$48719
R;Higashino, K.; Tshizaki, J.; Kishino, J.; Ohara, O.; Arita, H.
Eur. J. Biochem. 225, 375-382, 1994
A;Title: Structural comparison of phospholipase-A(2)-binding regions in phospholipase-A
A;Reference number: \$48719; MUD:95010128; PMID:7925459
A;Accession: \$48719
A;

Gaps .; 0 2; Length 1487; Query Match 86.0%; Score 43; DB Best Local Similarity 77.8%; Pred. No. 8; Matches 7; Conservative 1; Mismatches

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929 CSVPLPSIC 937 1 CSVPLTSVC 9 g à

probable membrane protein STY4229 [imported] - Salmonella enterica subsp. enterica serow
C)Species: 3almonella enterica subsp. enterica serowar Typhi
A,Note: this species has also been called Salmonella typhi
C,Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 18-Nov-2002
C,Accession: AD0990
R,Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher, t., T.; Connerton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar, S.; Moule, S.; O'Gaora, P.
Nature 413, 848-852, 2001
A;Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; A;Thite: Complete genome sequence of a multiple drug resistant Salmonella enterica seroy A;Reference number: AB0502; MUID:21534947; PMID:11677608
A;Accession: AD0990
A;Ataus: preliminary
A;Molecule type: DNA
A;Residues: 1-349 c-PAR>
A;Cross-references: GB:AL513382; PIDN:CAD08048.1; PID:g16505028; GSPDB:GN00176
C;Genetics:
A;Genetics:
A;Genetics:
A;Genetics:
A;Genetics:

Query Match

82.0%; Score 41; DB 2; Length 349;

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Whyothetical protein EC84323 [imported] - Escherichia coli (strain O157:H7, substrain R. C. Species: Bacherichia coli
C. Species: Bacherichia coli
C. Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 03-Aug-2001
C. Accession: C91169
R. Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G gaaswara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.
DNA Res: 8, 11-22, 2001
A, Reference number: A99629; MuID:21156231; PMID:11258796
A, Accession: C91169
A, Status: preliminary
A, Molecule type: DNA
A, Residues: 1-376 < HAX>
A, Residues: 1-376 < HAX>
A, Residues: 1-376 < HAX>
A, Cross-references: GB:DA00007; PIDN:BAB37746.1; PID:g13363797; GSPDB:GN00154
A, Experimental source: strain 0157:H7, substrain RIMD 0509952
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Best Local Similarity 100.0%; Pred. No. 5.3;
Matches 8; Conservative 0; Mismatches 0; Indels
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C,Superfamily: conserved hypothetical protein HI0338
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C,Superfamily: aspartate transaminase
C,Keywords: aminotransferase
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A) Reference number: 84766

A) Reference number: 84766

A) Reference number: 84766

A) Recession: 84763

A) Status: preliminary

A) Molecule type: DNA

A) Readules: 1-376 < PLD.

A) Rose, D.J.; Mau, B.; Shao, Y.

A) Rose, D.J.; Mau, B.; Shao, Y.

A) Relected to the complete genome sequence of Escherichia coli K-12.

A) Reference number: A64720; MUD:97426617; PMID:9278503

A) Reference number: B65144

A) Reterence number: B65
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Cydate: Instruction measurements of the control of 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             hypothetical protein yhhT [imported] - Escherichia coli (strain O157:H7, substrain EDL93
C;Species: Escherichia coli
C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 14-Sep-2001
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Best Local Similarity 100.0%; Pred. No. 5.3;
Matches 8; Conservative 0; Mismatches 0; Indels
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A;Start codon: GTG
C;Superfamily: conserved hypothetical protein HI0338
                     Pred. No. 4.9;
; Mismatches
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                          100.0%;
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Best Local Similarity 100.
Matches 8; Conservative
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Cispecies: Clostridium acetobutylicum (Species: Clostridium acetobutylicum (Species: Clostridium acetobutylicum (Species: Clostridium acetobutylicum (Species: Clostridium acetobutylicum (Spacies: Clostridium acetobutylicum (Spacession: D9710) (S.) Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Lee, S. Molling, J.; Breton, G.; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Lee, J. Bacteriol. 183, 4823-4838, 2001
S. Jacteriol. 183, 5000; MuID:21359325; PMID:21359325
S. Jacteriol. D97130
S. Jacteriol. 183, Markarova, M.S. Jacteriol. 1900; Markarova, Markarova, M.S. Jacteriol. 1900; Markarova, Markarova, Markarova, M.S. Jacteriol. 1900; Markarova, Mark
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C;Date: 31.May-1991 #sequence_revision 31-May-1991 #text_change 12-Apr-1995
C;Accession: A37931
R;Svendsen, I.; Nicolova, D.; Goshev, I.; Genov, N.
Carlsbherg Res. Commun. 54, 231-239, 1989
A;Title: Isolation and characterization of a trypsin inhibitor from the seeds of kohlrab A;Reference number: A37931; MUID:91202906; PMID:2490369
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                                                                            2073/1; 2098/2; 2146/3
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                                                    Aintrons: 400/2; 1608/3; 1644/1; 1674/3; 1686/2; 1731/2; 2073/1; 2098/2; C.Superfamily: LDL receptor ligand-binding repeat homology F:15-49/Domain: LDL receptor ligand-binding repeat homology cLDL3-F:51-85/Domain: LDL receptor ligand-binding repeat homology cLDL3-F:50-132/Domain: LDL receptor ligand-binding repeat homology cLDL3-F:90-132/Domain: LDL receptor ligand-binding repeat homology cLDL3-F:190-225/Domain: LDL receptor ligand-binding repeat homology cLDL3-F:190-225/Domain: LDL receptor ligand-binding repeat homology cLDL5-F:229-272/Domain: LDL receptor ligand-binding repeat homology cLDL5-F:369-405/Domain: LDL receptor ligand-binding repeat homology cLDL5-F:369-405/Domain: LDL receptor ligand-binding repeat homology cLDL9-F:969-903/Domain: LDL receptor ligand-binding repeat homology cLDL9-F:969-931/Domain: LDL receptor ligand-binding repeat homology cLDL3-F:908-943/Domain: LDL receptor ligand-binding repeat homology cLDL3-F:908-941/Domain: LDL receptor ligand-binding repeat homology cLD13-F:903-1027/Domain: LDL receptor ligand-binding repeat homology cLD13-F
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Pred. No. 2.2e+02;
1; Mismatches 0; Indels
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Matches 6; Conservative
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54 CSIGYTSVC 62
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Matches 6; Conserv
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A; Description: Cloning a CDPK from Chlamydomonas eugametos.
A; Reference number: 854788
A; Reference number: 854788
A; Status: preliminary
A; Molecule type: mRNA
A; Residues: 1-591 < SID>
A; Cross-references: EMBL: Z49233; NID: 9806541; PIDN: CAA89202.1; PID: 9806542
C; Superfamily: calcium dependent protein kinase; calmodulin repeat homology; protein kinase; LAF P; Calcium binding; EF hand; serine/threonine-specific protein kinase; tan F; 150-166/Region: protein kinase ATP-binding motif
F; 158-166/Region: protein kinase ATP-binding motif
F; 158-166/Region: protein kinase ATP-binding motif
C;Accession: B55538
R;Rich, J.J.; Kinscherf, T.G.; Kitten, T.; Willis, D.K.
Bacteriol. 176, 74684-7475, 1994
A;Title: Genetic evidence that the gacA gene encodes the cognate response regulator for A;Reference number: A55538; WIID:95095914; PMID:8002569
A;Accession: B5538
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-22 <RIC>
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C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 18-Aug-2000
C;Accession: T29764
R;Du, Z.; Le, T.T.
submitted to the EMBL Data Library, May 1997
A;Description: The sequence of C. elegans cosmid T21E3.
A;Pecession: T29764
A;Accession: T29764
A;Accession: T29764
A;Accession: T29764
A;Accession: T20881
A;Accession: T20881
A;Accession: T20881
A;Accession: T20881
A;Accession: T20881
A;Accession: T2080 cDUz>
A;Accession: T2080 cDUz>
A;Cross-references: EMBL:AF003133; PIDN:AABS4138.1; GSPDB:GN00019; CESP:T21E3.3
A;Genetics:
A;Genetics:
A;Genetics:
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554788
calcium-stimulated protein kinase - Chlamydomonas eugametos
C;Species: Chlamydomonas eugametos
C;Date: 08-Uul-1995 #sequence_revision 21-Jul-1995 #text_change 18-Jun-1999
C;Accession: S54788
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F.489-521/Domain: calmodulin repeat homology cEF2>
F.525-55//Domain: calmodulin repeat homology cEF3>
F.559-591/Domain: calmodulin repeat homology cEF3>
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Pred. No.
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66.7%;
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C,Genetics:
A,Gene: uvrC
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13 CSVPASTVC 21
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Best Local Similarity
Matches 6; Conserv
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Best Local Similarity
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allergen Sin a I (clone SINS) - white mustard (fragment)
C;Species: Sinapis alba (white mustard)
C;Species: Sinapis alba (white mustard)
C;Species: Sal-Oct-1996 #sequence_revision 13-Mar-1997 #text_change 16-Jul-1999
C;Accession: S65478
R;Gonzalez de la Pena, M.A.; Monsalve, R.I.; Batanero, B.; Villalba, M.; Rodriguez, R.; Biochem. 237, 827-882, 1996
A;Title: Expression in Escherichia coli of Sin a 1, the major allergen from mustard.
A;Reference number: S65478
A;Accession: S65478
A;Accession: S65478
A;Residues: nucleic acid sequence not shown
A;Molecule type: DNA
A;Residues: 1-145 <GONS
A;Residues: 1-145 <GONS
A;Residues: 1-145 <GONS
A;Residues: seed
C;Genetics:
A;Genetics:
A;Genetics:
A;Genetics:
A;Genetics:
C;Superfamily: wheat alpha-amylase inhibitor
C;Keywords: seed; storage protein
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C;Species: Sinapis alba (white mustard)
C;Species: Sinapis alba (white mustard)
C;Species: Soloci-1996 #sequence_revision 13-Mar-1997 #text_change 16-Jul-1999
C;Accession: 865481
R;Gonzalez de la Pena, M.A.; Monsalve, R.I.; Batanero, E.; Villalba, M.; Rodriguez, R. Bur, J. Biochem: 237, 827-832, 1996
A;Tile: Expression in Escherichia coli of Sin a 1, the major allergen from mustard. A;Reference number: 8654431
A;Accession: 865481
A;Accession: 866481
A;Accession: 86
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Pred. No. 28;
2; Mismatches 2; Indels
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Pred. No. 28;
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55.6%;
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55.6%;
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Best Local Similarity 55.6
Matches 5; Conservative
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les 5; Conservative
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Job time : 7.90909 secs
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114 CNIPQVSVC 122
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C;Superfamily
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     R;Menendez-Arias, L.; Moneo, I.; Dominguez, J.; Rodriguez, R.
Bur. J. Biochem. 177, 159-166, 1988
A;Title: Primary structure of the major allergen of yellow mustard (Sinapis alba L.) see
A;Reference number: S01791; MUID:89030681; PMID:3181153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C,Accession: A01330
R;Crouch, M.L.; Tenbarge, K.M.; Simon, A.B.; Ferl, R.
J. Mol. Appl. Genet. 2, 273-283, 1983
A;Title: CDNA Clones for Brassica napus seed storage proteins: evidence from nucleotide A;Reference number: A92836; MUID:84113267; PMID:6689334
A;Accession: A01330
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Allergen Sin a I - white mustard
N.Alternate names: allergen Sin a I large chain
C.Species: Sinapis alba (white mustard)
C.Date: 28-Oct-1996 #sequence_revision 13-Mar-1997 #text_change 17-Mar-1999
C.Accession: 865447; 801792
R.Gonzalez de la Pena, M.A.; Monsalve, R.I.; Batanero, E.; Villalba, M.; Rodriguez, Bur. J. Biochem. 237, 827-832, 1996
A.Title: Expression in Bscherichia coli of Sin a 1, the major allergen from mustard. A.Reference number: 865447; MUID:96235251; PMID:8647131
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NyAlternate names: 1.7S seed storage protein
C.Species: Brassica napus (rape)
C.Species: 18-Apr-1984 #sequence_revision 18-Apr-1984 #text_change 18-Jun-1999
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A;Residues: 1-133 <CRO.

A;Cross-traferences: GB:K01544; NID:g167174; PIDN:AAA33005.1; PID:g167175

A;Experimental source: cv. Tower

C;Superfamily: wheat alpha-amylase inhibitor

C;Superfamily: wheat alpha-amylase inhibitor

F;Reyworks: seed apin 1 small chain (fragment) #status predicted <SCH>

F;50-130/Product: napin 1 large chain #status predicted <LCH>
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A;Molecule type: protein
A;Residues: 40-127 <MEN>
C;Superfamily: wheat alpha-amylase inhibitor
C;Keywords: seed; storage protein
   A,Residues: 1-124 <SVE>
C,Superfamily: wheat alpha-amylase inhibitor
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A,Residues: 1-127 <GON>
A,Experimental source: seed
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GenCore version 5.1.6 (c) 1993 - 2004 Compugen Ltd. Copyright

OM protein - protein search, using sw model

5, 2004, 09:38:39; Search time 4.09091 Seconds (without alignments) 114.554 Million cell updates/sec September Run on:

US-09-761-636A-10 50

1 CSVPLTSVC 9 score: Sequence: BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

141681 segs, 52070155 residues Searched:

141681 Total number of hits satisfying chosen parameters:

DB seq length: 0 DB seq length: 200000000 Minimum I Maximum I

Post-processing: Minimum Match 0%

Maximum Match 100% Listing first 45 summaries

SwissProt 42:* Database : Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES Res

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NXF5 HUMAN G3PA_MAIZE GRUT BOVIN GRN2 HUMAN G3PB_PEA ALGB PSESM PXRG MYCCA NU5M_BRALA NU5M_BRALA NU5M BRAFL NXF1_COTJA
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ALIGNMENTS

STRAIN=0157:H7 / RIMD 0509952;
MEDLINE=21156231; PubMed=11258796;
Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoyama K., Han C.-G., Ohtsubo E., Nakayama K., Murata T., Tanaka M., Tobe T., Iida T., Takami H., Honda T., Sasakawa C., Ogasawara M., Yasunaga T., Kuhara S., Shiba T., Hattori M., Shinagawa H.; Scherichia coli "Complete genome sequence of enterohemorrhagic Escherichia coli 0157:H7 and genomic comparison with a laboratory strain K-12."; STRAIN=K12 / MG1655;
MEDLINE=94316500; PubMed=8041620;
Sofia H.J., Burland V., Daniels D.L., Plunkett G. III, Blattner F.R.;
"Analysis of the Escherichia coli genome. V. DNA sequence of the
region from 76.0 to 81.5 minutes.";
Nucleic Acids Res. 22:2576-2586(1994). "Genome sequence of enterohaemorrhagic Escherichia coli 0157:H7."; Nature 409:529-533(2001). Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales; Enterobacteriaceae; Escherichia. NCBI_TaxID=562, 83334; SEQUENCE FROM N.A.
STRAIN-0157.H7 / EDL933 / ATCC 700927;
MEDLINE=21074935, PubMed=11206551,
Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D.,
Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,
Posfai G., Hackett J., Klink S., Boutin A., Shao Y., Miller L.,
Grotbeck E.J., Davis N. W., Lim A., Dimalanta E.T., Potamousis K.,
Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C.,
Melch R.A., Blattner F.R., -!- SUBCELLULAR LOCATION: Integral membrane protein (Potential). -!- SIMILARITY: BELONGS TO THE UPF0118 (PERM) FAMILY. STRONG, TO H.INFLUENZAE H10338. YHHT ECOLI STANDARD; PRT; 349 AA. B37622; P76700; O8X6P3; O1-OCT-1994 (Rel. 30, Created) C1-OVT-1997 (Rel. 35, Last sequence update) 28-FEB-2003 (Rel. 41, Last annotation update) Hypothetical protein yhhT. YHHT OR B3474 OR Z4848 OR ECS4323. Escherichia coli, and Escherichia coli 0157:H7. SEQUENCE FROM N.A. STRAIN=K12 / MG165 SEQUENCE FROM N.A.

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SMART; SM00465; GIYC; 1.
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Rich J.J., Kinscherf T.G., Kitten T., Willis D.K.;

Rich J.J., Kinscherf T.G., Kitten T., Willis D.K.;

"Genetic evidence that the gada gene encodes the cognate response
"Genetic or the lema sensor in Pseudomonas syringae.";

J. Bacteriol. 176:7468-7475(1994).

-!-FUNCTION: The UVTABC repair system catalyzes the recognition and
processing of DNA lesions. UvrC both incises the 5' and 3' sides
of the lesion. The N-terminal half is responsible for the 3'
incision and the C-terminal half is responsible for the 5'
incision (By similarity).

-!- SUBUNIT: Interacts with uvrB in an incision complex (By
                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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28-FEB-2003 (Rel. 41, Last annotation update)
UVRABC system protein C (UvrC protein) (Excinuclease ABC subunit C)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pseudomonas syringae (pv. syringae).
Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
Pseudomonadaceae; Pseudomonas.
                                                                                                                                                                                                                                                                                                                                                                                                                                               0;
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                                                                                                                                                                              Transmembrane; Complete proteome.
                                                                                                                                                                                                                                                                                                                                                                275ADBAD4FD58257 CRC64;
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100.0%; Pred. No.
ive 0; Mismatch
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EMBL; AE000423; AAC76499.1; ALT INIT.
EMBL; AE005570; AAG58583.1; ALT INIT.
EMBL; AP002565; BAB37746.1; ALT INIT.
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InterPro; IPR000305; UvrC N.
Pfam; PF01541; Exci_endo_N; 1.
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15-JUL-1998 (Rel. 36, Last seq
28-FEB-2003 (Rel. 41, Last ann
                                                                                                                                                                                                                                                                                                                                                                  38522 MW;
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Pfam; PP01594; UPP0118; 1.
Hypothetical protein; Transmer
TRANSMEM 11 31
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Viridiplantae; Streptophyta; Entrophyta; Spermatophyta; Magnoliophyta; eurosida; core eudicots; rosids; eurosida II; Brassicales; Brassicaceae; Sinapis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Menendez-Arias L., Moneo I., Dominguez J., Rodriguez R.;
"Primary structure of the major allergen of yellow mustard (Sinapis alba L.) seed, Sin a I.";
Eur. J. Biochem. 177:159-166(1988).
-!- FUNCTION: This is a 25 seed storage protein.
-!- SUBGUIT: The protein consists of two chains linked by disulfide bonds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -!- ALLERGEN: Causes an allergic reaction in human. Causes cabbage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      allergy.
-!- SIMILARITY: Belongs to the 28 seed storage albumins family.
PIR; S01791; S01791.
PIR; S65447; S65447; S65447.
InterPro; IPR003612; AAI.
InterPro; IPR000617; Napin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .,
PROSITE; PS50164; UVRC_1; 1.
SOS response; Excision nuclease; DNA repair; DNA recombination;
                                                                                                                                                     ·;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 127;
                                                                                                              76.0%; Score 38; DB 1; Length 150; 66.7%; Pred. No. 1.5; 1; Indels iive 2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
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R -> G.
7 4CD920284F04EEFD CRC64;
                                                                          16999 MW; ACC38718B5F1E2B1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                    01-APR-1990 (Rel. 14, Created)
01-APR-1990 (Rel. 14, Last sequence update)
10-0CT-2003 (Rel. 42, Last annotation update)
Allergen Sin a 1, small and large chains (Sin a I).
Sinapis alba (White mustard) (Brassica hirta).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (Rel. 01, Created)
(Rel. 01, Last sequence update)
(Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 133 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB
                                                                                                                                                                                                                                                                                                                                       127 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; irrucco., prints; pro196; NAPIN.
ProDom; PD002498; Napin; 1.
SMART; SM0499; AAI; 1.
Allergen; Seed storage protein.
39 SMALL CHAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 35;
Pred. No. 5
                                                                                                                                                                                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TISSUE=Seed;
MEDLINE=89030681; PubMed=3181153;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             70.0%;
                                                                                                      Query Match
Best Local Similarity 66.7.
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les 5; Conservative
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13 CSVPASTVC 21
                                                                                                                                                                                                 1 CSVPLTSVC 9
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                                                                             SEQUENCE 150 AA;
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21-JUL-1986
16-OCT-2001
                                           excision
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P01091;
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from a precursor polypeptide.";
J. Mol. Appl. Genet. 2:273-283(1983).
-!- FUNCTION: The small, basic, water-soluble napins are one of the two major kinds of storage proteins synthesized in the seed during
                                                                                                                                                                                                                                                              Crouch M.L., Tenbarge K.M., Simon A.E., Ferl R.; "cDNA clones for Brassica napus seed storage proteins: evidence from nucleotide sequence analysis that both subunits of napin are cleaved
                                                                                                                    MEDLINE-87033665; PubMed-3771543;
Ericson M.L., Roedin J., Lenman M., Glimelius K., Josefsson L.-G.,
                                                                                                                                                              "Structure of the rapeseed 1.7 S storage protein, napin, and its
                                                              Josefsson L.-G.;
Submitted (JUL-1987) to the EMBL/GenBank/DDBJ databases.
                      Biol. Chem. 262:12196-12201(1987).
                                                                                                                                                                                          Biol. Chem. 261:14576-14581(1986)
                                                                                                                                                                                                                                   STRAIN=cv. Tower;
MEDLINE=84113267; PubMed=6689334;
                                                                                                                                                                                                                                                                                                                                                                 its maturation.
                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                      SEQUENCE FROM N.A.
          Brassica napus.";
                                                                                                                                                                               predursor.
                                                  REVISIONS
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PROPEP
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                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its muse by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                           J. Mol. Appl. Genet. 2:273-283 (1983).
-!- FUNCTION: The small, basic, water-soluble napins are one of the two major kinds of storage proteins synthesized in the seed during
                                                                                                                                                                                                                                                  -!- SUBUNIT: The mature protein consists of a small and a large chain linked by disulfide bonds.
-!- TISSUE SPECIFICITY: Cotyledons and the axis.
-!- SIMILARITY: Belongs to the 2S seed storage albumins family.
  Brassica napus (Rape).

Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; NCBI_TaxID=3708;
                                                                                                                                      Crouch M.L., Tenbarge K.M., Simon A.E., Ferl R., "CDNA clones for Brassica napus seed storage proteins: evidence from nucleotide sequence analysis that both subunits of napin are cleaved from a precursor polypeptide.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots, rosids, eurosids II, Brassicales, Brassicaceae, Brassica.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=87308224; PubMed=3624251;
Josefsson L.-G., Lenman M., Ericson M.L., Rask L.;
"Structure of a gene encoding the 1.7 S storage protein, napin, from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ·
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Pred. No. 5.3;
2; Mismatches 2; Indels
Napin 1 precursor (1.78 seed storage protein) (Fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LARGE CHAIN.
SFDFC7ECE3E22ACB CRC64;
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01-AUG-1992 (Rel. 23, Last annotation update)
Napin 2 precursor (1.78 seed storage protein)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   178 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR003612; AAI.
InterPro; IPR000617; Napin.
Pfam; PF00234; tryp alpha_amyl; 1.
PRINTS; PR00496; NAPIN.
ProDom; PR002498; Napin; 1.
SWART; SW00499; AAI; 1.
Seed storage protein; Multigene family.
                                                                                                             STRAIN=cv. Tower;
MEDLINE=84113267; PubMed=6689334;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                130 L
15294 MW;
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01-MAR-1989 (Rel. 10, Last seg
                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; K01544; AAA33005.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        70.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
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                                                                                                                                                                                                                                          its maturation.
                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             133 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         PIR; A01330;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0
-!- SUBUNIT: The mature protein consists of a small and a large chain linked by disulfide bonds.
-!- TISSUE SPECIFICITY: Cotyledons and the axis.
-!- SIMILARITY: Belongs to the 2S seed storage albumins family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ·.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     70.0%; Score 35; DB 1; Length 178; 55.6%; Pred. No. 7.2;
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S -> N (IN REF. 4).
734E561971B539FF CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Signal; Multigene family.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SMALL CHAIN.
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                                                                                                                                                                                                                                                                                                                                                                                                                                              Pfam; PF00234; tryp alpha_amyl;
PRINTS; PR00496; NAPIN.
ProDom; PD002498; Napin; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     38
74 SN
175
175
17
76
20104 MW;
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EMBL; J02586; AAA32997.1; -.
EMBL; J02798; AAA87348.1; -.
                                                                                                                                                                                                                                                                                                                                                               PIR; A01329; NWRP2.
PIR; A29801; A25997.
InterPro; IPR003612; AAI.
InterPro; IPR000617; Napin.
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Seed storage protein; S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CYTOPLASMIC (POTENTIAL).
SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
                                                                                                                                                                                                                                                                                                                                                                             -i. FUNCTION: Plays a role as a receptor for the recognition of MHC class I HLA-E molecules by NK cells and some cytotoxic T-cells.
-i. SUBUNIT: Can form disulfide-bonded heterodimer with CD94.
-i. SUBCELLULAR LOCATION: Type II membrane protein.
-i. TISSUB SPECIFICITY: Natural killer cells.
-i. SIMILARITY: Contains 1 C-type lectin family domain.
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C-TYPE LECTIN (LONG FORM).
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
N-LINKED (GLCKAC. .) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL, AF190943; AAF74539.1; -.
InterPro; IPR001304; Lectin_C.
Pfam; PF00059; Lectin_c; 1.
SMART; SM00034; CLECT; 1.
PROSITE; PSS0041; C_TYPE_LECTIN_2; 1.
Receptor; Transmembrane; Multigene family; Signal-anchor; Lectin;
                                                                                                                                        Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Cercopithecidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       21-JUL-1986 (Rel. 01, Created)
01-MAY-1991 (Rel. 18, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Tyrosinase precursor (EC 1.14.18.1) (Monophenol monooxygenase).
                                                                                                                                                                                                                                                                                             identification of novel transmembrane-deleted forms of NKG2-A, and D.";
28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
28-FEB-2003 (I integral membrane protein (NKG2-D activating NK receptor) (NK cell receptor D).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 1; Length 216;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A44883F31400DEAC CRC64;
                                                                                                                                                                                                                                                                MEDINE=20322487; PubMed=10866118;
ABDONTE M.L., Levy D.B., Letvin N.L.;
"Characterization of rhesus monkey CD94/NKG2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          620 AA.
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                                                                                                                                                                                                                                                                                                                                                                   Immunogenetics 51:496-499(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       25075 MW;
                                                                                                                           Macaca mulatta (Rhesus macaque)
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DOMAIN 1 51
TRANSMEM 52 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 55.0
Lag 5; Conservative
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                                                                                                                                                                                       Cercopithecinae; Macaca.
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203
115
131
163
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202 2
216 AA;
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                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                            NCBI_TaxID=9544;
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98
99
127
189
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TYRO_NEUCR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             induction of Brassica microspore embryogenesis.", plant Mol. Biol. 26:1711-1723(1994).
-!- FUNCTION: The small, basic, water-soluble napins are one of the two major kinds of storage proteins synthesized in the seed during its maturation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -!- SUBDINITY: The mature protein consists of a small and a large chain linked by disulfide bonds.
-!- TISSUE SPECIFICITY: Cotyledons and the axis.
-!- SIMILARITY: Belongs to the 2S seed storage albumins family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Boutilier K.A., Gines M.J., Demoor J.M., Huang B.,
Baszczynski C.L., Iyer V.N., Miki B.L.;
"Expression of the BnmNAP subfamily of napin genes coincides with the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots, rosids, eurosids II; Brassicales, Brassicaceae, Brassica.
                                                                                                                                                                                                                                                       STRAIN=cv. Westar; IISSUE=Leaf;
MEDLINE=21346654; PubMed=2102844;
Bassczynski C.L., Fallis L.;
Isolation and mucleotide sequence of a genomic clone encoding a new
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LARGE CHAIN.
6F3883CBED55FB26 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 35; DB 1;
Pred. No. 7.3;
2; Mismatches 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Seed storage protein; Signal; Multigene family.
                01-AUG-1990 (Rel. 15, Created)
01-AUG-1990 (Rel. 15, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
Napin precursor (1.78 seed storage protein).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      216 AA.
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InterPro; IPR000617; Napin.
Pfam; PF00234; tryp alpha_amyl; 1.
PRNUTS; PR00496; NAPIN.
ProDom; PD002498; Napin; 1.
SMART; SM00499; AAI; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=cv. Topas;
MEDLINE=95161697; PubMed=7858212;
                                                                                                                                                                                                                                                                                                                                          Brassica napus napin gene.";
Plant Mol. Biol. 14:633-635(1990)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2
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55.6%;
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CNIPQVSVC 169
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180 AA;
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5; Conserv
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                                                                                                                                                                                                    NCBI_TaxID=3708;
                                                                                                                         Brassica napus
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AC Q9MZJ7;
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its most by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
                                                                                                                                                                                                                                                                                                                       STRAIN-TS, and Sing;
MEDLINE=82190019; PubMed=6210697;
Ruegg C., Ammer D., Lerch K.;
Comparison of amino acid sequence and thermostability of tyrosinase from three wild type strains of Neurospora crassa.";
J. Biol. Chem. 257:6420-6426(1982).
-!- FUNCTION: THIS IS A COPPER-CONTAINING OXIDASE THAT FUNCTIONS IN THE FORMATION OF PIGMENTS SUCH AS MELANINS AND OTHER POLYPHENOLIC
                                                                                                                                                                                                                                           "Primary structure of tyrosinase from Neurospora crassa. II. Complete amino acid sequence and chemical structure of a tripeptide containing an unusual thioether.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COULD BE INVOLVED IN ENZYME ACTIVATION. ACETYLATION.
              Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Sordariomycetidae; Sordariales; Sordariaceae; Neurospora,
                                                                                                                                                                                                                                                                                                                                                                                                                                                      CATALYTIC ACTIVITY: L-tyrosine + L-DOPA + O(2) = L-DOPA +
                                                                                STRAIN=TS, and Oak Ridge;
MEDLINE=90008884; PubMed=2529259;
Kupper U., Niedermann D.M., Travaglini G., Lerch K.;
"Isolation and characterization of the tyrosinase gene from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR008922; Di-copper centre.
InterPro; IPR002227; Tyrosinase.
Pfam, PF00264; Lyrosinase; 1.
PRINTS; PR00092; TYROSINASE.
PROSITE; PS00499; TYROSINASE. 1; 1.
PROSITE; PS00498; TYROSINASE. 2; 1.
Melanin blosynthesis; Oxidoreductase; Monooxygenase; Copper;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COPPER A (BY SIMILARITY).
COPPER A (BY SIMILARITY).
COPPER B (BY SIMILARITY).
COPPER B (BY SIMILARITY).
COPPER B (BY SIMILARITY).
COPPER B (BY SIMILARITY).
2'-(S-cysteinyl)-histidine (C. T -> P (IN STRAIN OR).
D -> E (IN STRAIN SING).
E -> T (IN STRAIN SING).
KS -> NN (IN STRAIN SING).
I -> T (IN STRAIN SING).
K -> NN (IN STRAIN SING).
I -> T (IN STRAIN SING).
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COFACTOR: Binds 2 copper ions per subunit (By si
MISCELLANEOUS: THE STRAIN TS SEQUENCE IS SHOWN.
SIMILARITY: Belongs to the tyrosinase family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYROSINASE.
                                                                                                                                                         Biol. Chem. 264:17250-17258(1989).
                                                                                                                                                                                                                                                                                   Biol. Chem. 257:6414-6419(1982)
                                                                                                                                                                                                STRAIN=TL;
MEDLINE=82190018; PubMed=6210696;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; M32843; AAA33619.1; -.
EMBL; M33271; AAA33618.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Acetylation; Thioether bond.
INIT MET 0 0 0
CHAIN 1 407
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105
277
277
281
306
14
130
130
3346
423
                                                                                                                                        Neurospora crassa."
  Neurospora crassa.
                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                  SEQUENCE OF 1-407.
                                                                                                                                                                                                                                                                                                             SEQUENCE OF 1-407
                                          NCBI_TaxID=5141;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPOUNDS.
                                                                                                                                                                                                                           Lerch K.;
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similarity).

(Cys-His).

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R. STRAIN-CS7BL/60; TISSUB-Embryo;

RX MEDLINE-21085660; PubMed=11217851;

RA Kawai J., Shinadawa A., Shibata K., Yoshino M., Itch M., Ishii Y.,

RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,

RA Arakawa T., Hara A., Pukunishi Y., Konno H., Radachi J., Fukuda S.,

RA Aito T., Okazaki Y., Golobori T., Bono H., Kasukawa T., Saito R.,

Radota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,

RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,

RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,

RA Kadota K., Matsuda H.A., Ashburner M., Batalov B., Kochiwa H.,

RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,

RA Sakai K., Okido T., Furuno M., Carninci P., de Bonaldo M.F.,

RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,

RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,

RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,

Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,

RA Sasaki H., Sato K., Schoenbach C., Seya T., Shakamoto N.,

RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,

Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,

M. Puntzional annotation of a full-length mouse cDNA collection.",
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RX SEQUENCE FROM N.A.

RX SEQUENCE FROM N.A.

RX STAUSBETST; PubMed=12477932;

RA STAUSBETST R.L., Feingold B.A., Grouse L.H., Derge J.G.,

RA Altschul S.F., Zeeberg B., Bueden E.M., Schaefer C.F., Bhat N.K.,

RA HOPKINS R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Mullahy S.J.,

RA Brownstein M.J., Nckwan P.J., McKernan K.J., Malek J.A., Gunarane P.H.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Villalon D.K., Muxny D.W., Sodergren B.J., Lu X., Gibbs R.A.,

RA Witting W., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

RA Rodriguez A.C., Grimwood J., Schwutz J., Dickson M.C.,

RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

RA Rodriguez A.C., Grimwood J., Schmutz J., Mayers R.M.,

RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;

RY Generation and initial analysis of more than 15,000 full-length

RY Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                                                         SYR MOUSE STANDARD; PRT; 660 AA.
09D019; QBVDM1;
28-FEB-2003 (Rel. 41, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Arginyl-tRNA synthetase (EC 6.1.1.19) (Arginine--tRNA ligase) (ArgRS).
                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                       ..
                                                                                             70.0%; Score 35; DB 1; Length 620; 75.0%; Pred. No. 27; 1ve 2; Mismatches 0; Indels
449 449 K -> R (IN STRAIN OR).
234 234 N -> D (IN REF. 2 AND 3).
620 AA; 68546 MW; D12A30BB6A01D312 CRC64;
                                                                                                                                               6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nature 409:685-690(2001).
                                                                                                                                                                                                                                          589 TVPLTSLC 596
                                                                                                                                                                                          2 SVPLTSVC 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mus musculus (Mouse)
                                                                                                                 Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=10090;
                    CONFLICT
                                                                                             Query Match
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Matches
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SMART; SM00499; AAI; 1.
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SEQUENCE
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                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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Monsalve R.I., Gonzalez de la Pena M.A., Menendez-Arias L.,
Lopez-Octin C., Villalba M., Rodríquez R.;
"Characterization of a new oriental-mustard (Brassica juncea)
allergen, Bra j IE: detection of an allergenic epitope.";
Biochem J. 293:425-631(1993).
- !- FUNCTION: This is a 28 seed storage protein.
- SUBUNIT: THE MATURE PROTEIN CONSISTS OF A SMALL AND A LARGE CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IrNO 1110, IRNO 1110, IRNA-8ynt_Id_C.
InterPro; IPR0008909; IRNA-8ynt_Id_C.
InterPro; IPR001412; tRNA-8ynt_Id_T.
Pfam; PF00748; IRNA-8ynt_Id; 1.
Pfam; PF007546; IRNA-8ynt_Id; 1.
Priority; PR01038; TRNASYNTHARG.
TIGRRAMS; TIGR00456; args; 1.
TIGRRAMS; TIGR00456; args; 1.
TIGRRAMS; TIGR00456; args; 1.
TIGRRAMS; TIGR00456; args; 1.
TIGRAMS; TIGRO 1110, IRNA_INGARE 1.
TIGRAMS; TIGRO 1110, IRNA_INGARE 1.
TIGRAMS; TIGRO 1110, IRNA_INGARE 1.
TIGR
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P80207; P80215;
01-0CT-1993 (Rel. 27, Created)
01-0CT-2003 (Rel. 27, Last sequence update)
10-0CT-2003 (Rel. 42, Last annotation update)
Allergen Bra j 1-E, small and large chains (Bra j I).
Brassica juncea (Leaf mustard) (Indian mustard).
Brassica juncea (Leaf mustard) (Indian mustard).
Spermatophyta; Magnoliophyta; eudicocyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicacea; Brassica.
NUBL TaxID=3707;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                    diphosphate + L-arginyl-tRNA(Arg).
-!- SUBUNIT: Monomer; also part of a multisubunit complex that groups tRNA ligases for Arg, Asp, Glu, Gln, Ile, Leu, Lys, Met and Pro.-:- SUBCELLUMAR LOCATION: Cytcoplasmic.
-!- DOMAIN: The N-terminal (AA 1-72) has two regions predicted to be alpha-helical that might be involved in the multisynthetase
                                                                                                                                                                                                                                            -:- SIMILARITY: Belongs to class-I aminoacyl-tRNA synthetase family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ;
                  CATALYTIC ACTIVITY: ATP + L-arginine + tRNA(Arg) = AMP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 1; Length 660;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MULTISYWTHETASE COMPLEX.
"HIGH" REGION.
L. -> H (IN REF. 1).
G -> V (IN REF. 1).
M -> L (IN REF. 1).
W, 6E8EBCC590FABBID CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 35;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; AK011383; BAB27583.1; -.
EMBL; BC020132; AAH20132.1; -.
MGD; MG1:1914297; Rars.
InterPro; IPR001278; Arg_tRNA-synt_lc.
InterPro; IPR005148; N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pred.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           70.0%;
87.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity 87.5
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  369 CSVPLTIV 376
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178 1
210 2
474 4
660 AA;
                                                                                                                                                                                                                             complex assembly
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CONFLICT
SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           sequence motif.";
Eur. J. Biochem. 197:741-746(1991).
-!- FUNCTION: The small, basic, water-soluble napins are one of the
two major kinds of storage proteins synthesized in the seed during
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -!- SUBUNIT: The mature protein consists of a small and a large chain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots, rosids, eurosids II; Brassicales, Brassicaceae, Brassica.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ericson M.L., Muren E., Gustavsson H.O., Josefsson L.G., Rask L.; "Analysis of the promoter region of napin genes from Brassica napus demonstrates binding of nuclear protein in vitro to a conserved
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     linked by disulfide bonds.
-!- TISSUE SPECIFICITY: Cotyledons and the axis.
-!- SIMILARITY: Belongs to the 2S seed storage albumins family.
               -i- SIMILARITY: Belongs to the 2S seed storage albumins family. PIR; S35591; S35591. InterPro; IPR003612; AAI. InterPro; IPR003617; Napin. PRINTS; PR00496; Napin. PRODM; PR002498; Napin. 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               68.0%; Score 34; DB 1; Length 129; 44.4%; Pred. No. 8.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                    6 6 F -> I.
20 20 R -> K.
129 AA; 14644 MW; D6F28E03F62B08F8 CRC64;
-!- ALLERGEN: Causes an allergic reaction in human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-AUG-1992 (Rel. 23, Created)
01-AUG-1992 (Rel. 23, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Napin B precursor (1.78 seed storage protein)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT; 178 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3; Mismatches
                                                                                                                                                                                                                                                                                                                              LARGE CHAIN.
F -> I.
R -> K.
                                                                                                                                                                                                                                                                        SMALL CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pfam; PF00234; tryp alpha amyl; 1. PRINTS; PR00496; NAPIN. ProDom; PD002498; Napin; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
STRAIN-cv. Svalofs Karat 20516-K;
MEDLINE-91231016; PubMed=2029903;
                                                                                                                                                                                                   SMART; SM00499; AAI; 1.
Allergen; Seed storage protein.
CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL, X58142; CAA41150.1; -.
PIR, S15382; S15382.
InterPro; IPR003612; AAI.
InterPro; IPR000617; Napin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 44.*.
A Conservative
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                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mol. Microbiol. 16:977-989(1995)
-!- FUNCTION: PROBABLY INVOLVED IN POLYMERIZATION AND/OR EXPORT OF
EXOPOLYSACCHARIDE EPS I WHICH FUNCTIONS AS A VIRULENCE FACTOR.
-!- SUBCELLULAR LOCATION: Integral membrane protein. Outer membrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pfam; PF02563; Poly export; 1.
PROSITE; PS00013; PROKAR_LIPOPROTEIN; FALSE_NEG.
Polysaccharide transport; Transport; Outer membrane; Transmembrane; Lipoprotein; Porin; Signal; Palmitate.
SIGNAL 1. 23 POTENTIAL.
                                                                                                                                                                                                                                                                                                                 01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
10-CCT-2003 (Rel. 42, Last annotation update)
EPS I polysaccharide export outer membrane protein epsA precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Molécular characterization of the eps gene cluster of Pseudomonas solanacearum and its transcriptional regulation at a single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   palmitoyl cysteine (By similarity). BE0084252E819309 CRC64;
                                                                                                                                                           .;
0
                                                                                                                                                                                                                                                                                                                                                                                                              Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EPS I POLYSACCHARIDE EXPORT OUTER MEMBRANE PROTEIN EPSA.
                                                                                                                        Score 34; DB 1; Length 178;
Pred. No. 11;
                 BY SIMILARITY.
BY SIMILARITY.
SMALL CHAIN (BY SIMILARITY).
                                                                          LARGE CHAIN (BY SIMILARITY). 96CE0ADB7CD966E9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      S-diacylglycerol cysteine (By
                                                                                                                                                         Indels
   Signal; Multigene family; Embryo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -:- SIMILARITY: BELONGS TO THE BEXD/CTRA/VEXA FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                           Ralstonia solanacearum (Pseudomonas solanacearum)
                                                               BY SIMILARITY.
                                                                                                                                                      Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   similarity).
N-palmitoyl o
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PIR; S77634; S77634.
InterPro, IPR003715; Poly export.
InterPro, IPR000437; Prok_lipoprot_S.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=96059643; PubMed=7476194;
                                                                                        20114 MW;
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                                                                                                                        68.0%;
55.6%;
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                                                                                                                                                                                                                                                                                                                                                                                                                           Burkholderiaceae; Ralstonia.
                                                                                                                                                    5; Conservative
                                                                                                                                                                                                                                                                                         STANDARD:
                  21
38
74
94
178
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Seed storage protein;
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                                                                                          178 AA;
                                                                                                                      Query Match
Best Local Similarity
                                                                                                                                                                               1 CSVPLTSVC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              377 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=305;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  24
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                                                                                                                                                                                                                                                                                        EPA2 RALSO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   promoter."
                                                                                          SEQUENCE
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                                                            PROPEP
                              PROPEP
               SIGNAL
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                                             CHAIN
                                                                          CHAIN
                                                                                                                                                                                                                                                                        RALSO
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MEDLINE=22486644; PubMed=12488443; Miggin S.M., Lawler O.A., Kinsella B.T.; Miggin S.M., Lawler O.A., Kinsella B.T.; Palmitoylation of the human prostacyclin receptor. Functional implications of palmitoylation and isopremylation."; J. Biol. Chem. 278:6947-6958(2003).
-! FUNCTION: Receptor for prostacyclin (prostaglandin I2 or PGI2).
-The activity of this receptor is mediated by G(s) proteins which activitae adenylate cyclase.
-! SUBCELLULAR LOCATION: Integral membrane protein.
-: SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nakagawa O., Tanaka I., Usui T., Harada M., Sasaki Y., Itoh H., Yoshimasa T., Namba T., Narumiya S., Nakao K.; "Molecular cloning of human prostacyclin receptor cDNA and its gene expression in the cardiovascular system."; Circulation 90:1643-1647(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
MEDLINE=95394450; PubMed=7665161;
Ogawa Y., Tanaka I., Inoue M., Yoshitake Y., Isse N., Nakagawa O., Usui T., Itoh H., Yoshimasa T., Narumiya S.;
"Structural organization and chromosomal assignment of the human
                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Warren C.N., Aronstam R.S., Sharma S.V., "CDNA clones of human proteins involved in signal transduction sequenced by the Guthrie cDNA resource center (www.cdna.org)."; Submitted (FEB-2003) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=94216334; PubMed=7512962;
Boie Y., Rushmore T.H., Darmon-Goodwin A., Grygorczyk R.,
Slipetz D.M., Metters K.M., Abramovitz M.;
"Cloning and expression of a cDNA for the human prostanoid IP
                                                                                                                                                                          01-NOV-1995 (Rel. 32, Last sequence update)
15-WAR-2004 (Rel. 43, Last annotation update)
Prostacyclin receptor (Prostanoid IP receptor) (RGI receptor)
(Prostaglandin I2 receptor).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Narumiya S., Ichikawa A.; "Cloning and expression of a cDNA for the human prostacyclin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
MEDLINE=94237286; PubMed=7514139;
Katsuyama M., Sugimoto Y., Namba T., Irie A., Negishi M.,
Narumiya S., Ichikawa A.;
                                                                                                                         386 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Biol. Chem. 269:12173-12178(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TISSUE=Lung;
MEDLINE=95008086; PubMed=7923647;
                                                                                                                                                            Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            prostacyclin receptor gene.";
Genomics 27:142-148(1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FEBS Lett. 344:74-78(1994).
                                                                                                                         STANDARD;
                         16 CAVPLMAAC 24
                                                                                                                                                   01-NOV-1995 (Rel. 32, 01-NOV-1995 (Rel. 32,
                                                                                                                                                                                                                                                            Homo sapiens (Human)
1 CSVPLTSVC
                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IISSUE=Placenta;
                                                                                                                                                                                                                                             PTGIR OR PRIPR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PALMITOYLATION
                                                                                                                                                                       01-NOV-1995
15-MAR-2004
                                                                                                                                                                                                                                                                                                                                                                   TISSUE=Lung;
                                                                                                                       HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               receptor
                                                                                                                                        P431\overline{19}
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Gaps

·,

2; Indels

2; Mismatches

5; Conservative

Local Similarity

Best Loca Matches

Score 34; DB 1; Length 377; Pred. No. 25;

68.0%; 55.6%;

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                                                                                                                                               MIM; 600022; -. 6000289; C:integral to plasma membrane; TAS. 60; G0:0005897; E:prostaglandin I receptor activity; TAS. 60; G0:0004959; F:prostaglandin I receptor activity; TAS. 60; G0:0007267; P:cell-cell signaling; TAS. 60; G0:0007187; P:G-protein signaling; coupled to cyclic nucl. . ; TAS. InterPro; IPR000276; ProstanoidR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CIKS HUMAN STANDARD; PRT; 574 AA.
043734; Q9HSW2; Q9HSY3; Q9NS14; Q9UG72;
16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Adapter protein CIKS (Connection to IKK and SAPK/JNK) (Nuclear factor NP-kappa-B activator 1) (ACT1).
                                                                                                                                                                                                                                   PROSITE; PS00237; G PROTEIN RECEP F1 1; 1.
PROSITE; PS50262; G PROTEIN RECEP F1 2; 1.
G-protein coupled receptor; Transmembrane; Glycoprotein; Lipoprotein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                       (POTENTIAL)
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0
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                                                                                                                                                                                                                                                                                                                                                                             EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                 4 (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                            LINKEH (GLUNAC. . .) (F)
2B6B0CDBACED1608 CRC64;
                                                                                                                                                                                                                                                                                                      EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                                                                                                                     EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                       7 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                        CYTOPLASMIC (POTENTIAL).
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                                                                                                                                                                                                                                                                                      (POTENTIAL) .
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S-palmitoyl cysteine.
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                                                                                  Pfam; PF00001; 7tm 1; 1.
PRINTS; PR00237; GPCRRHODOPSN.
PRINTS; PR01788; PROSTANOIDR.
                                                                                                                                                                                                                                                                                                                                                                                                                                 40955 MW;
                                                                          EMBL; L29016; AAA36448.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity 66.7
Matches 6; Conservative
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251 CSLPLTIRC 259
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SEQUENCE
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RX MEDILE=2238827; PubMed=12477932;

RX MEDINE=2238827; PubMed=12477932;

RA Altausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

RA Altschul S.F., Zeeberg B. Buercow K.H., Schaefer C.F., Bahat N.K.,

RA Hopkins R.P., Jordan H., Moore T., Mang J., Haish F.,

RA Hopkins R.P., Jordan H., Moore T., Mark S.I., Wang J., Haish F.,

RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

RA Raha S.A., MocEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

RA Raha S.A., MocEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

RA Raha S.A., Motewan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

RA Rahay J., Helton E., Ketteman M., Soderia A.M., Gay L.J., Hulyk S.W.,

RA Pakey J., Helton E., Ketteman M., Soderia B.J., Lu X., Gibbs R.A.,

RA Blakesley R.W., Touchman J.W., Schevchenko Y., Bouffard G.G.,

RA Butterfield Y.S.M., Krzywinski M.I., Skalska U., Smailus D.E.,

RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;

RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;

RA Schnerch and initial analysis of more than 15,000 full-length

RY Winan and mouse cDNA sequences.";

Ry Generation and initial analysis of more than 15,000 full-length

RY Human and mouse cDNA sequences.";

Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).

Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).

Proc. Natl. Prepapa-B inhibitor kinase (IKK)-dependent mechanism and stress-activated protein kinase (IKK)-dependent mechanism and with IKBKB/IKK-beta.

CHUK/IKK-alpha and with IKBKB/IKK-beta.

CHUK/IKK-alpha and with IKBKB/IKK-beta.
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                                                                                                                                                                            "Cloning and characterization of two overlapping genes in a subregion at 6q21 involved in replicative senescence and schizophrenia."; Gene 252:217-225(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Leonardi A., Chariot A., Claudio E., Cunningham K., Siebenlist U., "CIKS, a connection to Ikappa B kinase and stress-activated protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     <u>.</u>
                                                                                                                                                                                                                                                                                                                                                                                                           TISSUE=Embryonic kidney;
MEDLINE=20442402; PubMed=10962024;
Li X., Commane M., Nie H., Hua X., Chatterjee-Kishore M., Wald I. Haag M., Stark G.R.;
"Actl, an NF-kappa B-activating protein.";
Proc. Natl. Acad. Sci. U.S.A. 97:10489-10493(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TISSUE=12764,
MEDLINE=20442403; PubMed=10962033;
Transard: a. Charlot A., Claudio E., Cunningham K., Siebenlist
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Submitted (MAY-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (FEB-1998) to the EMBL/GenBank/DDBJ databases
                                                           MEDLINE-20363742; PubMed-10903453;
Morelli C., Magnanini C., Mungall A.J., Negrini M.,
Barbanti-Brodano G.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Proc. Natl. Acad. Sci. U.S.A. 97:10494-10499 (2000)
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Name=1; Synonyms=C60RF4;
[1] SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A. (ISOFORM 2).
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inhibitor.";
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                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to licenseeisb-sib.ch).
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10-OCT-2003 (Rel. 42, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
CDK5 regulatory subunit associated protein 1 (CDK5 activator-binding protein C42).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Rattus.
NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=21975289; PubMed=11882646;
Ching Y.-P., Pang A.S.H., Lam W.-H., Qi R.Z., Wang J.H.;
"Identification of a neuronal Cdk5 activator-binding protein as Cdk5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HELIX-LOOP-HELIX MOTIF (BY SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /FIId=VSP_004163.
Q -> H (IN REF. 1; AAF67445, 2 AND 4).
E -> D (IN REF. 3; AAF67447).
MISSING (IN REF. 6; BAB15117).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=20184747; PubMed=10721722;
Ching Y.-P., Qi Z., Wang J.H.;
"Cloning of three novel neuronal Cdk5 activator binding proteins.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        68.0%; Score 34; DB 1; Length 574;
85.7%; Pred. No. 40;
1: Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GG; GO:0007242; P:intracellular signaling cascade; NAS. Alternative splicing.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               64657 MW; E9857DEA5E349094 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       586 AA.
                  Name=2; Synonyms=C6ORF5,
IsoId=O43734-2; Sequence=VSP_004163;
TISSUE SPECIFICITY: Widely expressed.
  IsoId=043734-1; Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                                              EMBL, AF274303, AAG15367.1, ...
EMBL, AF272151, AAG15407.1, ...
EMBL, AL008730, CAA15506.1, ...
EMBL, AL008730, CAA15507.1, ALT_INIT.
EMBL, AL050289, CA43390.1, ...
EMBL, AK025551, BAB15117.1, ...
EMBL, AK025531, AAH02823.1, ...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Missing (in
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EMBL; AF136406; AAF67446.1; -.
EMBL; AF136407; AAF6747.1; -.
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Best Local Similarity 85.79,
--hos 6; Conservative
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Genew; HGNC:1343; C6orf4.
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574 AA;
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225 LPLTSVC 231
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ID AC Q9JUH
DT 10-OC
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DE CDKS.

OC BARTHU
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1. Biol. Chem. 277:15237-15240(2002).

2. -!- FUNCTION: Probable regulator of CDKS activity. May inhibit CDKS cluncion via its interaction with CDKSR1.

2. -!- SUBDNIT: Interacts with CDKSR1 and CDKSR2.

2. -!- SUBDNIT: Interacts with CDKSR1 and CDKSR2. The interaction with CDKSR1 is prevented by the association between CDKSR1 and CDKSRAP2. Interacts also with the complex CDKSR1-CDKS. Does not interact with monomeric CDKS. The interaction is prevented by the association between CDKSR1 and CDKSRAP2.

2. -- DOMAIN: The C-terminal part (475-586) is necessary for the interaction with CDKSRAP1, while the N-terminal part (1-168) is required for inhibiting the activity of the CDKS kinase.

2. -- SIMILARITY: Belongs to the UPP0004 family. CDKSRAP1 subfamily.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 1; Length 586; 41;
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InterPro; IPR007463; MidB_methiolase.
InterPro; IPR007197; Radical_SAM.
InterPro; IPR007192; TRAM.
InterPro; IPR005639; UPP0004.
Pfam; PF04055; Radical_SAM; 1.
Pfam; PF00919; UPF0004; 1.
SMART; SM00729; Blp3; 1.
TIGRPAMs; TIGR01574; miaB-methiolase; 1.
TIGRPAMs; TIGR01699; TIGR00089; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               68.0%; Score 34; DB 75.0%; Pred. No. 41; ive 1; Mismatches
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PROSITE; PSG1926; TRAM; 1.
PROSITE; PSG128; UPP0004; 1.
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les 6; Conservative
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Job time : 6.09091 secs
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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protein search, using sw model OM protein -

5, 2004, 09:46:09; Search time 20.3636 Seconds (without alignments) 139.448 Million cell updates/sec September Run on:

US-09-761-636A-10 50 Perfect score:

BLOSUM62 Scoring table:

1 CSVPLTSVC 9

Sequence:

Gapop 10.0 , Gapext 0.5

1017041 seqs, 315518202 residues Searched:

1017041 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SPTREMBL Database

sp archa: *
sp bacteria: *
sp bugi: *
sp fung: *
sp human: *
sp nammal: *
sp mammal: *
sp organelle: * unclassified:* sp_virus:* sp_vertebrate:* sp_plant:* sp_rodent:* rvirus:* Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

sp_bacteriap:*

sp archeap:*

Description	Q62028 mus musculu Q8228 salmonella Q8228 salmonella Q8228 salmonella Q8228 salmonella Q8239 o shigella fil Q81791 rattus sp. Q8772 arabidopsis Q9276 lycopersico Q9arc6 lycopersico Q9arc6 lycopersico Q9arga arabidopsis Q91094 arabidopsis Q91094 arabidopsis Q91094 arabidopsis Q91094 arabidopsis Q91094 methanococc Q8wvw3 homo sapien Q9h671 homo sapien Q9h747 homo sapien
SUMMARIES	062028 Q8ZLE3 Q8ZLE3 Q8ZJE9 Q8JJG0 Q8FCN4 Q8FCN4 Q8ARXR2 Q9ARXR2 Q9ARRF2 Q9ARRF2 Q9LG04 Q9LG04 Q9BTQ4 Q9HGR1
DB	1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
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ALIGNMENTS

Mus musculus (Mouse). Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. AN HIGH SEQUENCE FROM N.A.

REDINES SEQUENCE FROM N.A.

RA Higashino K., Ishizaki J., Kishino J., Ohara O., Arita H.;

RA Higashino K., Ishizaki J., Kishino J., Ohara O., Arita H.;

RI "Structural comparison of phospholipase-A2-binding regions in phospholipase-A2 receptors from various mammals.";

RI BL J. Blochem. 225:375-382(1994).

BR BL, J. Blochem. 225:375-382(1994).

BR BR, S48719; S48719.

BR MGI:102466; Pla2glbr.

BR MGI:102466; Pla2glbr.

CO: 00:0005529; F:sugar binding; IEA.

BR MGI:102466; Pla2glbr.

CO: 00:005529; F:sugar binding; IEA.

BR MGI:102466; Pla2glbr.

CO: 00:005529; F:sugar binding; IEA.

BR MGI:102466; Pla2glbr.

BR MGI:102466; Pla2glbr.

BR InterPro; IPR00059; Firein Blike.

BR FAM: PR00059; FWI:2; I.

BR PRIMIS: PR00013; FWIYPE II; I.

BR SWART; SW00059; FWI:1; I.

BR SWART; SW00059; FWI:1.

BR SWART; SW00458; RICIN; I.

BR PROSITE; PS50041; C_TYPE LECTIN_2; 8. 01-NOV-1996 (TrEMBLrel. 01, Created) 01-NOV-1996 (TrEMBLrel. 01, Last sequence update) 01-OCT-2003 (TrEMBLrel. 25, Last annotation update) PRT; 1487 AA. Phospholipase A2 receptor precursor. PRELIMINARY; NCBI_TaxID=10090; Q62028 Q62028; RESULT 1 262028

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2 SVPLTSVC 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bacteria, Proteobacteria, Gammaproteobacteria, Enterobacteriales,
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Enterobacteriaceae; Salmonella.
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                                                                   DB 11; Length 1487;
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Pred. No. 4.4;
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                            SIGNÄL 1 26 POTENTIAL.
CHAIN 27 1487 PHOSPHOLIPASE AZ RECEPTOR.
SEQUENCE 1487 AA; 170511 MW; ADBD905859B0EDE8 CRC64;
                                                                                       1; Indels
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InterPro, IPR002549; UPP0118.
Pfam, PR01594; UPP0118.
Hypothetical protein; Complete proteome.
SEQUENCE 349 Aa, 38301 MW; 21A55D9F2C5FDB9A CRC64;
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Last sequence update)
Last annotation update)
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(TrEMBLrel. 20, Last Sequence update)
(TrEMBLrel. 21, Last annotation update)
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                                                                    Score 43; DB 1
Pred. No. 6.5;
1; Mismatches
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  PS50231; FICIN_B_LECTIN; 1.
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NCEL_TaxID=601;
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01-MAR-2002 (TrEMBLrel. 20, Cr
01-MAR-2002 (TrEMBLrel. 20, La
01-JUN-2002 (TrEMBLrel. 21, La
Putative Perm family permease.
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Best Local Similarity luv..
'-, 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                     Nature 413:852-856(2001).
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                                                                                         7; Conservative
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                                                                                                                                                                                                                                                   Salmonella typhimurium
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                                                                      Query Match
Best Local Similarity
                  Receptor; Signal.
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Salmonella typhi
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  PROSITE;
PROSITE;
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STRAIN=301 / Serotype 2a;
MEDLINE=22272406; PubMed=12384590;
Jin Q., Yuan Z., Xu J., Wang Y., Shen Y., Lu W., Wang J., Liu H.,
Jin Q., Yuang F., Zhang X., Zhang J., Yang G., Wu H., Qu D., Dong J.,
Sun L., Xue Y., Zhao A., Gao Y., Zhu J., Kan B., Ding K., Chen S.,
Cheng H., Yao Z., He B., Chen R., Ma D., Qiang B., Wen Y., Hou Y.,
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Parkhill J., Dougan G., James K.D., Thomson N.R., Pickard D., Wain J. Churcher C., Mungall K.L., Bentley S.D., Holden M.T.G., Sebaihia M., Baker S., Basham D., Brooks K., Chillingworth T., Connerton P., Cronin A., Davis P., Davies R.M., Dowd L., White N., Farrar J., Feltwell T., Hamin N., Haque A., Hen T.T., Holroyd S., Jagels K., Krogh A., Larsen T.S., Leather S., Moule S., O'Gaora P., Parry C., Quail M., Rutherford K., Simmonds M., Skelton J., Stevens K., Whitehead S., Barrell B.G., Whitehead S., Barrell B.G., Barrell B.G., Eather S., Moule S., O'Gaora P., Parry C., Whitehead S., Barrell B.G., B
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STRAIN=2457T / ATCC 700930 / Serctype 2a;
STRAIN=2457T / ATCC 700930 / Serctype 2a;
STRAIN=245074; PubMed=12704152;
Weblink=22590274; PubMed=12704152;
Weblink=20404 M.B., Burland V., Venkatesan M.M., Deng W.,
Fournier G., Mayhew G.F., Plunkett G. III, Rose D.J., Darling A.,
Schwartz D.C., Blattner F.R.,
"Complete genome sequence and comparative genomics of Shigella
"Complete genome sequence and comparative genomics of Shigella
Ilearer: serctype 2a strain 2457T.";
Infect. Immun. 71:2772-2786 (2003).
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Bacteria, Proteobacteria, Gammaproteobacteria, Enterobacteriales,
Enterobacteriaceae, Shigella.
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01-JUN-2003 (TrEMBLrel. 24, Created)
01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-JUN-2003 (TrEMBLrel. 25, Last annotation update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
0rf, conserved hypothetical protein (Hypothetical protein yhhT).
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GO, GO:0004872; F:receptor activity; IEA.
GO; GO:0005529; F:sugar binding; IEA.
InterPro.; IFRO:1014; Lectin_C.
Pfam; PF00059; lectin_C; 3.
SMART; SM00034; CLECT; 3.
PROSITE; PSE0041; C_TYPE_LECTIN_Z; 3.
                        Eur. J. Biochem. 225:375-382(1994).
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                                         EMBL; D30781; BAA06445.1; -. HSSP; P23807; 11XX.
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X MEDLINE=22388234; PubMed=12471157;
A Welch R.A., Burland V., Plunkett G. III, Redford P., Roesch P.,
A Machon B., Buckles E.L., Liou S.-R., Boutin A., Hackett J., Stroud D.,
A Mayhew G.F., Rose D.J., Zhou S., Schwartz D.C., Perna N.T.,
A Mobley H.L.T., Donnenberg M.S., Blattner F.R.;
A Mobley H.L.T., Donnenberg M.S., Blattner F.R.;
XT "Extensive mosaic structure revealed by the complete genome sequence R. L. Donnenberg M.S., Blattner F.R.;
XT of uropathogenic Escherichia coli.";
Proc. Natl. Acad. Sci. U.S.A. 99:17020-17024(2002).
R EMBL, AED16768; AAN22703.1;
DR FILE*Pro. IPR002549; UPF0118.
DR Ffam, PF01594; UPF0118; 1.
KW Hypothetical protein; Complete protecome.
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
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Enterobacteriaceae; Escherichia.
NCBI_TaxID=217992;
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MEDLINE=95010128; PubMed=7925459;
Higashino K., Ishizaki J., Kishino J., Ohara O., Arita H.;
"Structural comparison of phospholipase-A2-binding regions in phospholipase-A2 receptors from various mammals.";
                                                                                                                                        Length 349;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              82.0%; Score 41; DB 16; Length 376; 100.0%; Pred. No. 4.7;
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EMBL; AE016992; AAP19231.1; -.
InterPro; IPR002549; UPP0118.
Pfam; PF01594; UPF0118; 1.
Hypothetical protein; Complete proteome.
SEQUENCE 349 AA; 38464 MW; 935ADBA85BD65651 CRC64;
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100.0%; Pred. No. 4.4;
ive 0; Mismatches 0
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01-NOV-1996 (TrEMBLrel. 01, Last seq
01-OCT-2003 (TrEMBLrel. 25, Last ann
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Best Local Similarity 100.v.
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Matches 8; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=10118;
                                                                                                                                   Query Match
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                                                                                                                                                                                                                                                                                                                                                                                     Q8FCN4;
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                                                                                                                                                                                                                                                                                                                       RESULT 5
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063791
1D 06379
AC 06373
DT 01-NO
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Yamada K., Liu S.X., Sakano H., Pham P.K., Banh J., Chung M.K.,
A Goldsmith A.D., Lee J.M., Ouach H.L., Toriumi M., Yu G., Bowser L.,
A Garninci P., Chen H., Cheuk R., Hayashizaki Y., Ishida J., Jones T.,
A Carninci P., Chen H., Cheuk R., Hayashizaki Y., Ishida J., Jones T.,
A Kamiya A., Karlin-Neumann G., Kawai J., Kim C., Lam B., Lin J., Jones T.,
A Miranda M., Narusaka M., Nguyen M., Palm C.J., Sakurai T., Satou M.,
A Seki M., Shinn P., Southwick A., Shinozaki K., Davis R.W., Ecker J.R.,
A Theologis A.,
Theologis A.,
Thabidopsis Full Length cDNA Clones.";
Submitted (FBB-2002) to the EMBL/GenBank/DDBJ databases.
BR GO: GO:0016020; C:membrane; IEA.
BR GO: GO:0016020; C:membrane; IEA.
BR GO: GO:0006247; F:Voltage-gated chloride channel activity; IEA.
                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; edicotyledons; core eudicots; rosids;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
NCBI_TaxID=3702;
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                                                                82.0%; Score 41; DB 11; Length 409; 66.7%; Pred. No. 5.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             82.0%; Score 41; DB 10; Length 585; 100.0%; Pred. No. 7; tive 0; Mismatches 0; Indels
                                                                                                                                   Indels
409 AA; 47740 MW; 56D957D2DCA00AD8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRINTS; PR00762; CLCHANNEL.
SMART; SM00116; CBS; 2.
Hypochetical protein.
SEQUENCE 585 AA; 62547 MW; E29CE5844B81D826 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                 585 AA
                                                                                                                             2; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Arabidopsis thaliana (Mouse-ear cress).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR000644; CBS domain.
InterPro; IPR001807; Cl-Channel volt.
Pfam; PF00571; CBS; 2.
Pfam; PF00654; voltage CLC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
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ID 0
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Hypothetical protein.
SEQUENCE 750 AA; 79985 MW; 928E6D1EE2ESFCD4 CRC64;
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                                                                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        82.0%; S
100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRINTS; PR00762; CLCHANNEL, SMART; SMO116; CBS; 2.
Hypothetical protein.
                                                                          82.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 100.
Matches 8; Conservative
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                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          l protein.
780 AA; B
                                                                                                                                                                                                               474 CSVPLTSV 481
                                                    Query Match
Best Local Similarity
Best Local 8; Conserva
                                                                                                                                                                  1 CSVPLTSV 8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=81985;
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01-OCT-2003 (TrEWBLrel: 25, Last annotation update)
11-OCT-2003 (TrEWBLrel: 25, Last annotation update)
12-OCT-2003 (TrEWBLrel: 25, Last annotation update)
13-OCT-2003 (TrEWBLr
                                                    01-JUN-2001 (TIEMBLrel. 17, Last sequence update)
01-OCT-2003 (TIEMBLrel. 25, Last annotation update)
Hypothetical protein.
Lycopersicon esculentum (Tomato).
Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
lamiids; Solanales; Solanaceae; Solanum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Rossberg M., Theres K., Acarkan A., Herrero R., Schmitt T., Schumacher K., Schmitz G., Schmidt R., "Comparative sequence analysis reveals extensive microcolinearity in the Lateral supressor regions of the tomato, Arabidopsis and Capsella
                                                                                                                                                                                                                                                                      MEDLINE-21178822; PubMed-11283350; Rerrero R., Schmitt T., Rosabberg M., Theres K., Acarkan A., Herrero R., Schmitt T., Schumacher K., Schmitt R., Schumacher K., Schmitt R., "Comparative sequence analysis reveals extensive microcolinearity in the lateral supressor regions of the tomato, Arabidopsis and Capsella
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Plant Cell 13:979-988(2001).
Plant Cell 13:979-988(2001).
GO; GO:0016020; C:membrane; IEA.
GO; GO:0005247; F:voltage-gated chloride channel activity; IEA.
GO; GO:0006821; P:chloride transport; IEA.
Interpro; IPR000644; CBS domain.
Interpro; IPR01807; Cl-channel_volt.
PF00571; CBS; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL, AJ303344, CAC36399.1; -.. GO, GO: 0016020; C:membrane; IEA. GO; GO: 0016020; C:membrane; IEA. GO; GO: 001624; F:voltage-gated chloride channel activity; IEA. GO; GO:0006821; F:voltage-gated chloride transport; IEA. InterPro; IPR000644; CBS domain. InterPro; IPR001807; Cl-channel_volt.
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Pred. No. 8.8;
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01-JUN-2001 (TrEMBLrel. 17, Created)
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                                           01-JUN-2001 (TrEMBLrel. 17, Created)
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PRINTS; PR00762; CLCHANNEL.
SMART; SM00116; CBS; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pfam; PF00571; CBS; 2.
Pfam; PF00654; voltage CLC; 1.
PRINTS; PR00762; CLCHANNEL.
SMART; SM00116; CBS; 2.
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Plant Cell 13:979-988(2001).
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                                                                                                                                                                                                                              NCBI TaxID=4081;
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Matches
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01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2001 (TrEMBLrel. 25, Last annotation update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Hypothetical protein (CLC-f chloride channel protein).
Arabidopsis thaliana (Mouse-ear cress).
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
eurosids II Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                         01-UTN-2001 (TrEMBLrel. 17, Created)
01-UTN-2001 (TrEMBLrel. 17, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Capsella rubella.
Capsella rubella.
Eukaryota, Viidiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
eurosids II; Brassicales; Brassicaceae; Capsella.
                                                                  Gaps
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MEDLINE=21178822; PubMed=11283350;
Rossberg M., Theres K., Acarkan A., Herrero R., Schmitt T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 41, DB 10; Length 780; Pred. No. 9.2; 0; Mismatches 0; Indels
Length 750;
                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       83811 MW; 5718FA7E2AEE81FB CRC64;
                                                                     0;
      Score 41; DB 10;
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EMBL, AJ303349; CAC36391.1; -.

EMBL, AJ303349; CAC36391.1; -.

GO; GO:000520; C:membrane; IEA.

GO; GO:0005247; F:voltage-gated chloride char

GO; GO:0006821; P:chloride transport; IEA.

InterPro; IPR001664; CBS domain.

InterPro; IPR001607; Cl-channel_volt.

Pfam; PF00571; CBS; 2.

Pfam; PF00654; voltage_CLC; 1.
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                                           8.8
                                                                                                                                                                                                                                                                                                                                                                 780 AA
                                    100.0%; Preα. No. - ive 0; Mismatches
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Gonzalez A.A., Hansen N.N.F., Huizar L.L., Kremenetskaia I.I.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-OCT-2003 (TrEMBLrel. 25, Hypothetical protein MJ1479.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Methanococcus jannaschii.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 CSVPLTSV 8
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                                                                                                                                                          [5]
SEQUENCE FROM N.A.
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                                                                                                                                               28 SEQUENCE FROM N.A.

29 SEQUENCE FROM N.A.

20 TISSUE-Seedling aerial parts;

20 All Anauger-Loouard M., Charon C., Lapous D., Allot M., Granier F.,

21 RA Vinauger-Loouard M., Charon C., Lapous D., Allot M., Granier F.,

22 RA Abaldopsis chloride channel.";

23 "Molecular and functional characterization of AtCLC-f, a putative new

24 RABIGARD AND COLOGIDE CHANNEL.";

25 RBL; AND COLOGIDE CACCIONAL CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ·.
                            "Comparative sequence analysis reveals extensive microcolinearity in the Lateral supressor regions of the tomato, Arabidopsis and Capsella
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Arabidopsis thaliana (Mouse-ear cress).
Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
NCBI_TaxID=3702;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.

Khan S., Brooks S., Buehler E., Chao Q., Johnson-Hopson C., Kim C., Shinn P., Altafi H., Bei Q., Chin C., Chiou J., Choi E., Conn L., Conway A., Gonzales A., Hansen N., Howng B., Koo T., Lam B., Lee J., Lenz C., Li J., Liu A., Liu K., Liu S., Mukharsky N., Nguyen M., Palm C., Pham P., Sakano H., Schwartz J., Southwick A., Thaveri A., Ecker J.R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Genomic sequence for Arabidopsis thaliana BAC F20N2 from chromosome
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Shinn P.P., Buehler E.E., Dunn P.P., Feng J.J., Kim C.C., Li Y.Y.,
Walker M.M., Altafi H.H., Araujo R.R., Conn L.L., Conway A.A.B.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (AUG-1998) to the EMBL/GenBank/DDBJ databases.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           781 AA; 83548 MW; BE9DEB3603D9E0D8 CRC64;
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Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             784 AA.
  Schumacher K., Schmitz G., Schmidt R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pfam; PF00654; voltage CLC; 1.
                                                                                                         Plant Cell 13:979-988(2001).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRINTS; PR00762; CLCHANNEL.
SMART; SM00116; CBS; 2.
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les 8; Conserv
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SEQUENCE FROM N.A.
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Matches
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09LG04
DD C09LG0
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DT 01-OC
DD C01-OC
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A SEQUENCE FROM N.A.

A Cheuk R., Shinn P., Brooks S., Buehler E., Chao Q., Johnson-Hopson C.,
A Khan S., Kim C., Altafi H., Bei B., Chin C., Chiou J., Choi E.,
RA Conn L., Corway A., Gonzalez A., Hansen N., Howing B., Koo T., Lam B.,
RA Conn L., Corway A., Gonzalez A., Hansen N., Howing B., Koo T., Lam B.,
RA Lee J., Lenz C., Li J., Liu J., Liu J., Liu S., Mukharsky N.,
RA Thaveri A., Toriuni M., Vaysberg M., Yu G., Davis R., Federspiel N.,
RA Theologis A., Ecker J.;
Submitted (JUN-2000) to the EMBL/GenBank/DDBJ databases.
BR EMBL; AC002128; AAF79509.1; -.
BR GO; GO:0005247; Fivoltage-gated chloride channel activity; IEA.
BR GO; GO:0005247; Fivoltage-gated chloride channel activity; IEA.
BR GO; GO:0005821; P:chloride transport; IEA.
BR GO; GO:0005644; CBS domain.
BR InterPro; IPR000644; CBS domain.
BR Ther-Pro; IPR000644; CBS domain.
BR PRONT; SM00116; CBS; 2.
BR PRINTS; PR00564; Voltage CLC; 1.
BR RINTS; RN00116; CBS; 2.
BR PRINTS; RN00116; CBS; 2.
BR PRINTS; RN00116; CBS; 2.
Lenz C.C., Li J.J., Liu S.S., Luros S.S., Rowley D.D., Schwartz J.J., Tortumi M.W., Vysockaia V.V., Yu G.G., Davis R.R.W., Federspiel N.N.A., Theology A.A., Ecker J.J.R., Submitted (DEC-1998) to the EMBL/GenBank/DDBJ databases.
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STRAIN-JAL-1 / DSM 2661 / ATCC 43067;
MEDLINE=96337999; Pubmed=8688087;
Bult C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D., Sutton G.G., Blake J.A., FitzGerald L.M., Clayton R.A., Gocayne J.D., Sutton G.G., Blake J.A., FitzGerald L.M., Clayton R.A., Gocayne J.D., Scriton G.G., Rikness B.F., Weinstock K.G., Merrick J.M., Glodek A., Scott J.L., Geoghagen N.S.M., Weidman J.F., Puhrmann J.L., Nguyen D., Utcerback T.R., Kalley J.M., Peterson J.D., Sadow P.W., Hanna M.C., Cotton M.D., Roberts K.M., Hurst M.A., Kaine B.P., Borodovsky M., Klenk H.-P., Fraser C.M., Smith H.O., Woese C.R., Venter J.C., "Complete genome sequence of the methanogenic archaeon, Methanococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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                                                                                                                                                                                                                                        Ecker J.R.;
Submitted (MAY-2000) to the EMBL/GenBank/DDBJ databases.
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100.0%; Pred. No. 9.2
cive 0; Mismatches
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R GO; GO:0005622; C:intracellular; IEA.

GO; GO:0005840; C:ribosome; IEA.

R GO; GO:0005841; F:l-aminocyclopropane-1-carboxylate synthase . . .; IEA.

R GO; GO:0003735; F:structural constituent of ribosome; IEA.

R GO; GO:0003881; F:losynthesis IEA.

R GO; GO:0006412; P:protein biosynthesis; IEA.

R GO; GO:0006412; P:protein biosynthesis; IEA.

R HEEPPO; IPRO0439; Aminotrans I/II.

R HEEPPO; IPRO0529; Ribosomal $\overline{5}6$.

R Fam; PRO0155; aminotran 1.2; 1.

R Fam; PRO0155; aminotran 1.2; 1.

R PROSITE; PS01048; RIBOSOMAL $\overline{5}6$.

R PROSITE; PS01048; RIBOSOMAL $\overline{5}6$.
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Kawabata A., Hikiji T., Kobatake N., Inagaki H., Ikema Y., Okamoto S.,
Okitani R., Ota T., Suzuki Y., Obayashi M., Nishi T., Shibahara T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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01-WAR-2001 (TYEWBLrel. 16, Last sequence update)
01-OCT-2003 (TYEWBLrel. 25, Last annotation update)
4-YOPOTHERICAL PROTEIN FL/21969.
Homo sapiens (Human).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates; Catarrhini, Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-MRR-2002 (TrEWBLrel. 20, Created)
01-MAR-2002 (TrEWBLrel. 20, Last sequence update)
01-OCT-2003 (TrEWBLrel. 25, Last annotation update)
Hypothetical protein (Fragment).
How sapiens (Human).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata; Euteleostomi;
Mammalia; Eutheria, Primates; Catarrhini, Hominidae; Homo.
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Pred. No. 13;
0; Mismatches 2; Indels
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Strausberg R.;
Strausberg R.;
Submitted (2004-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC017468; AAH17468.1; -..
InterPro; IRR008928; Glyco_trans_6hp.
Hypothetical protein.
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77.8%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 78.0
Best Local Similarity 77.8
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
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Best Local Similarity
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Q8WVW3;
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RA Tanaka T., Nakamura Y., Isogai T., Sugano S.;

RT "NEDO human cDNA sequencing project.";

RL Submitted (AUG-2000) to the EMEL/GenBank/DDBJ databases.

BR EMBL; AK025622; BAB15192.1; -.

BR EMBL; AK025622; BAB15192.1; -.

BR Interpro; IRF008928; Glyco_trans_6hp.

KW Hypothetical protein.

SQ SEQUENCE 491 AA; 54720 MW; 4F73721A9D092C37 CRC64;

Query Match

Ouery Match

Authoritative 66.7%; Pred. No. 24;

Best Local Similarity 66.7%; Pred. No. 24;

Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps

Qy 1 CSVPLTSVC 9

Qy 1 CSVPLTSVC 9

A75 CSVPITDPC 483

Search completed: September 5, 2004, 10:00:01

Job time: 22.3636 secs.
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5, 2004, 09:37:49; Search time 29.5455 Seconds
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86.068 Million cell updates/sec
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GenCore version 5.1.6 (c) 1993 - 2004 Compugen Ltd.
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                                                                                                                                                                                                                                                                                1586107 seqs, 282547505 residues
                                                             protein search, using sw model
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50
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Maximum DB seq length: 200000000
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                 Copyright
                                                                                                September
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                                                                                                                                                                             Perfect score:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution. geneseqp1980s;*
geneseqp1990s;*
geneseqp2000s;*
geneseqp2001s;*
geneseqp2001s;* geneseqp2003as:* geneseqp2003bs:* geneseqp2004s:*

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Geneseq_29Jan04:*

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SUMMARIES	ID	AAU04529	AAB23826	AAU63687	ABM60206	AAU53277	ABM49796	AAU43894	ABM40413	AAU74551	ABG11475	AAB74693	AAE01782	ABG64141	ADASCRAR	ADA40695	ABD47707	ADC740BE	ADD37860	AB-T04424	DATE DACO	ADME 4000	ABM54988	ABB67846	ABP06465	AAG74036	AAU21569
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26	27	28	29	30	31	32	33	34	35	36	37	38	0 0	υ.	40	41	42	43	::	44	4.5	

ALIGNMENTS

Human, VEGF, vascular endothelial growth factor; angiogenesis; neovascularisation; lymphangiogenesis; psoriasis; tumour; diabetes induced neovascular sequelae; rheumatoid arthritis; diabetic retinopathy; chronic inflammation; cyclic. /note= "This bond cyclises the peptide" Cendron A; Location/Qualifiers 1..9 Stacker S, AAU04529 standard; peptide; 9 AA. VEGF based monocyclic peptide 7. (LUDW-) LUDWIG INST CANCER RES. 18-JAN-2001; 2001WO-US001533. 18-JAN-2000; 2000US-0176293P. 16-MAY-2000; 2000US-0204590P. (first entry) Hughes RA, WPI; 2001-442248/47. Key Disulfide-bond WO200152875-A1. 26-SEP-2001 26-JUL-2001. Synthetic. AAU04529; Achen MG, AAU04529

Novel monomeric monocyclic peptide, used to interfere with angiogenesis, or lymphangiogenesis, is produced by cyclizing a peptide loop fragment from an exposed loop of a growth factor protein by oxidizing the cysteine residues.

Claim 49; Page 32; 102pp; English.

The sequence represents a monomeric monocyclic peptide of the invention, whose 3-dimensional structure is modelled on the expose loop of human VEGFD (vascular endothelial growth factor). The invention relates to a method of producing a monomeric monocyclic peptide by a measuring betabeta carbon separation distances on opposite antiparallel strands of a

peptide loop fragment from an exposed loop of a growth factor protein and cyclising the peptide by oxidising the cysteine residues. The monocyclic peptides and a cyclic peptides (comprising 2 linked monocyclic peptides) and a cyclic peptide with at least one amino acid deleted prior to cyclisation are used to interfere with angiogenesis.

To cyclisation are used to interfere with angiogenesis.

To cyclisation are used to interfere with angiogenesis.

The condition is diabetic retinopathy, psoriasis, arthropathy, corpuraterised by angiogenesis, neovascularisation or lymphangiogenesis.

The condition is diabetic retinopathy, psoriasis, arthropathy, cerebrovascular accident, post-angioplasty restenosis, head, heat or cold trauma, substance-induced meovascularisation of the liver, excessive cramma, substance-induced meovascularisation of the liver, excessive cramma, propertension induced neovascular sequelae, hypertension induced neovascular sequelae, or chronic liver sequelae, hypertension induced neovascular excessive corputation. The peptides are also used to modulate vascular permeability in a mammal (the mammal has a condition characterised by fluid accountation in peripheral limbs or in lungs, peritoneal cavity, pleura, or brain. The peptides are used to image blood vessels and lymphatic or brain. The peptides are used to inage blood vessels and lymphatic vasculature. The monomeric and bicyclic peptides are used to interfere continuation in the peptides are used to condition with at least one biological activity induced by VEGF. VEGF-C or -D and care also used in combination with an anti-inflammatory agent, to treat a chronic inflammation, especially rheumatoid arthritis, psoriasis and diabetic retinopathy

Sequence 9 AA;

Gaps 6 100.0%; Score 50; DB 4; Length 9; 100.0%; Pred. No. 1.4e+06; ive 0; Mismatches 0; Indels 9; Conservative Query Match Best Local Similarity Matches 9; Conserv

; 0

1 CSVPLTSVC 9

ò g

CSVPLTSVC 9

RESULT 2 AAB23826

AAB23826 standard; protein; 1487 AA.

AAB23826;

(first entry) 15-JAN-2001

Murine phospholipase A2 receptor protein SEQ ID NO:7.

Endocytic C lectin family, E-selectin; type C lectin; identification.

Mus sp.

US6117977-A.

12-SEP-2000.

97US-00840062. 24-APR-1997; 96US-0052524P. 96US-00637021. 24-APR-1996; 24-APR-1996;

(GETH) GENENTECH INC.

WPI; 1997-535838/49.

Lasky LA;

Νu Κ,

Human and mouse type C lectin(s) - useful as competitive inhibitor of lectin activity and as molecular markers for tissues that express them

Example; Fig 3; 72pp; English.

The present invention describes an isolated type C lectin polypeptide (I) comprising amino acid residues 37-133, 37-174, 175-229, 234-360, 381-507, 520-645, 657-809, 884-951, 970-1108, 1110-1243, or 1259-1393 of the protein sequence given in AAB23822. The first 2 polypeptides are capable of binding to a carbohydrate residue, and the rest of the polypeptides

Sequences AAU39105-AAU68017 represent Propionibacterium acnes immunogenic polypeptides. The proteins and their associated DNA sequences are used in the treatment, prevention and diagnosis of medical conditions caused in P. acnes. The disorders include SAPHO syndrome (synovitis, acne, pustulosis, hypertosis and osteomyelitis), uveitis and endophthalmitis. P. acnes is also involved in infections of bone, joints and the central nervous system, however it is particularly involved in the inflammatory lesions associated with acne vulgaris. A method for detecting the are useful for producing antibodies capable of binding to these 2 polypeptides. Polynucleotide sequence encoding the polypeptides of the invention are useful in the identification and purification of their native ligands, and as molecular markers of the tissues in which they are expressed. They provide valuable sequence motifs, which can be inserted or substituted into other native members of the endocytic type C lectins, and provide hybridisation probes for searching cDNA and genomic libraries for the coding sequence of other type C lectins. Variants of type C lectins may be used therapeutically as competitive inhibitors of the biological activity of native type C lectins. The present sequence represents a murine phospholipase A2 receptor protein which is homologous to a type C lectin ó SAPHO syndrome; synovitis; acne; pustulosis; hypertosis; osteomyelitis; uveitis; endophthalmitis; bone; joint; central nervous system; ELISA; inflammatory lesion; acne vulgaris; enzyme linked immunosorbent assay; dermatological; osteopathic; neuroprotectant. Propionibacterium acnes polypeptides and nucleic acids useful for vaccinating against and diagnosing infections, especially useful for Gaps 0; Length 1487; Bhatia A; 1; Indels Propionibacterium acnes immunogenic protein #24583. Persing DH, Mitcham JL, Wang SS, e J, Zhang Y, Jen S, Carter D; 86.0%; Score 43; DB 2; I 77.8%; Pred. No. 1.3e+02; iive 1; Mismatches 1; Example 1; SEQ ID NO 24882; 1069pp; English. AAU63687 standard; protein; 73 AA 21-APR-2000; 2000US-0199047P. 02-JUN-2000; 2000US-0208841P. 07-JUL-2000; 2000US-0216747P. 20-APR-2001; 2001WO-US012865. (first entry) Query Match Best Local Similarity 77.8-Propionibacterium acnes. treating acne vulgaris. 929 CSVPLPSIC 937 WPI; 2001-616774/71. 1 CSVPLTSVC 9 CORI-) CORIXA CORP L'maisonneuve J, Sequence 1487 AA; N-PSDB; AAS59634 WO200181581-A2. 01-NOV-2001. 27-FEB-2002 Skeiky YAW, AAU63687; AAU63687 g à

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presence or absence of P. acnes in a patient comprises contacting a sample with a binding agent that binds to the proteins of the invention and determining the amount of bound protein in the sample. The polypeptides may be used as antigens in the production of antibodies specific for P. acnes proteins. These antibodies can be used to downregulate expression and activity of P. acnes polypeptides and therefore treat P. acnes infections. The antibodies may also be used as diagnostic agents for determining P. acnes presence, for example, by enzyme linked immunosobbent assay (ELISA). Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                       Propionibacterium acnes predicted ORF-encoded polypeptide #24882.
                                                                                                                                                                                                                                                                                                                                                                                                                                Acne vulgaris; antiseborrhoeic; dermatological; antibacterial;
                                                                                                                                                                                             Score 39; DB 4; Length 73;
Pred. No. 32;
1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                              immunostimulant; immune response; vaccine
                                                                                                                                          ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                               ABM60206 standard; protein; 73 AA.
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66.7%;
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Best Local Similarity 66.79,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Propionibacterium acnes.
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                                                                                                                                                                 Sequence 73 AA;
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Bhatia A, Benson DR, Skeiky YAW, Persing DH, ang S, Jen S, Lodes MJ, (CORI-) CORIXA CORP. Mitcham Jl, Zhang Y, Barth B,

Maisonneuve JL; Jones R, Carter D; Wang S, Jen S, Lode Vallieve-Douglass J; WPI; 2003-381789/36.

N-PSDB; ACF64563

New Propionibacterium acnes polypeptides and polynucleotides encoding the polypeptide, useful for diagnosing, preventing or treating acne vulgaris, or for stimulating an immune response specific for a P. acnes protein. Example 1; SEQ ID NO 24882; 1481pp; English.

The invention relates to an isolated polynucleotide (ACF64435-ACF64733) encoding a Propionibacterium acnes protein. The invention also relates to polypeptides encoded by the polynucleotides (ABM35624-ABM64536) and to additionally encompasses expression vectors and host cells comprising a polynucleotide of the invention, antibodies against polypeptides of the invention, polynucleotide of the invention; an immune response specific for a P. acnes polypeptide and an isolated T cell population comprising T cells prepared via this method; a vaccine composition (comprising P. acnes polypeptides, a vaccine composition (comprising P. acnes polypeptides, antibodies, fusion proteins, T cell populations, or

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antigen-presenting cells that express the polypeptide); a method and kit for detecting or determining the presence or absence of P. acnes in a patient; and amethod for inhibiting the development of P. acnes in a patient. The P. acnes polypeptides, polynucleotides, antibodies, fusion proteins, T cell populations or antigen-presenting cells that express the Colypeptides are useful for diagnosing, preventing or treating acne vulgaris, or for stimulating an immune response specific for a P. acnes protein. The polynucleotides can also be used as probes or primers for nucleic acid hybridisation. The vaccine composition is useful for the stimulation of an immune response against P. acnes, or for treating acne, and the kit is useful for performing a diagnostic assay. The present cand the kit is useful for performing a diagnostic assay. The present cading frame) contained within the P. acnes polynucleotides of the cinvention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pot_sequences
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Sequence 73 AA;

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Gaps

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Gaps
                    ;
  Length 73;
                   2; Indels
Score 39; DB 6;
Pred. No. 32;
1; Mismatches
78.0%;
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Best Local Similarity
                                  1 CSVPLTSVC
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9
                Matches
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43

CRAPITSVC

35

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AAU53277 standard; protein; 88

Ā

AAU53277;

27-FEB-2002 (first entry)

Propionibacterium acnes immunogenic protein #14173.

SAPHO syndrome, synovitis, acne, pustulosis; hypertosis; osteomyelitis, uveitis; endophthalmitis; bone, joint, central nervous system; ELISA, inflammatory lesion; acne vulgaris; enzyme linked immunosorbent assay; dermatological; osteopathic; neuroprotectant.

Propionibacterium acnes.

WO200181581-A2.

01-NOV-2001.

20-APR-2001; 2001WO-US012865.

21-APR-2000; 2000US-0199047P. 02-JUN-2000; 2000US-0208841P. 07-JUL-2000; 2000US-0216747P.

(CORI-) CORIXA CORP.

Bhatia A; Mitcham JL, Wang SS, , Jen S, Carter D; Persing DH, M L'maisonneuve J, YAW, Skeiky

2001-616774/71. N-PSDB; AAS59559 Propionibacterium acnes polypeptides and nucleic acids useful for vaccinating against and diagnosing infections, especially useful for treating acne vulgaris.

Example 1; SEQ ID NO 14472; 1069pp; English.

Sequences AAU39105-AAU68017 represent Propionibacterium acnes immunogenic polypeptides. The proteins and their associated DNA sequences are used in the treatment, prevention and diagnosis of medical conditions caused by P. acnes. The disorders include SAPHO syndrome (synovitis, acne,

pustulosis, hypertosis and osteomyelitis), uveitis and endophthalmitis.

P. acnes is also involved in infections of bone, joints and the central nervous system, however it is particularly involved in the inflammatory lesions associated with acne vulgaris. A method for detecting the presence or absence of P. acnes in a patient comprises contacting a sample with a binding agent that binds to the proteins of the invention and determining the amount of bound protein in the sample. The polypeptides may be used as antigens in the production of antibodies of specific for P. acnes proteins. These antibodies can be used to down-equilate expression and activity of P. acnes polypeptides and therefore treat P. acnes infections. The antibodies may also be used as diagnostic agents for determining P. acnes presence, for example, by charge linked immunosorbent assay (BLISA). Note: The sequence data for this patent did not form part of the printed specification, but was obtained in alectronic format directly from WIPO at the vipo.int/pub/published_pot_sequences Score 39; DB 4; Length 88; Pred. No. 39; 2; Indels 1; Mismatches 78.0%; 66.7%; Local Similarity 66.7 ses 6; Conservative Sequence 88 AA; Query Match Best Loc Matches

51 σ 1 CSVPLTSVC CSIPLTKPC à g

ABM49796 standard; protein; 88 AA. ABM49796; ABM4979(RESULT

Propionibacterium acnes predicted ORF-encoded polypeptide #14472. Acne vulgaris; antiseborrhoeic; dermatological; antibacterial; immunostimulant; immune response; vaccine (first entry) Propionibacterium acnes. 20-0CT-2003

11-OCT-2002; 2002WO-US032727. WO2003033515-A1. 24-APR-2003.

15-OCT-2001; 2001US-00978825. (CORI-) CORIXA CORP.

Mitcham JL, Skeiky YAW, Persing DH, Zhang Y, Wang S, Jen S, Lodes MJ,

Zhang Y, Wang S, Jen S, Lode Barth B, Vallieve-Douglass J;

WPI; 2003-381789/36. N-PSDB; ACF64488. New Propionibacterium acnes polypeptides and polynucleotides encoding the polypeptide, useful for diagnosing, preventing or treating acne vulgaris, or for stimulating an immune response specific for a P. acnes protein.

Example 1; SEQ ID NO 14472; 1481pp; English.

The invention relates to an isolated polymucleotide (ACF64435-ACF64733) encoding a Propionibacterium acnes protein. The invention also relates to polypeptides encoded by the polymucleotides (ABM35624-ABM64536) and to immunogenic fragments of P. acnes polypeptides. The invention additionally encompasses expression vectors and host cells comprising a polymucleotide of the invention, antibodies against polypeptides of the invention; invention; fusion proteins comprising a polypeptide of the invention; a

method for stimulating an immune response specific for a P. acnes polypeptide and an isolated T cell population comprising T cells prepared to polypeptide and an isolated T cell population cells a cones polypeptides, via this method; a vaccine composition (comprising P. acnes polypeptides, or polymucleotides); a method and kit antigen-presenting cells that express the polypeptide); a method and kit cantigen-presenting or determining the presence or absence of P. acnes in a patient; and a method for inhibiting the development of P. acnes in a patient. The P. acnes polypeptides, polymucleotides, antibodies, fusion proteins, T cell populations or antigen-presenting cells that express the proteins, or for stimulating an immune response specific for a P. acnes polypeptides are useful for diagnosing, preventing or treating acnes to protein. The polymucleotides can also be used as probes or primers for nucleic acid hybridisation. The vaccine composition is useful for the stimulation of an immune response against P. acnes, or for treating acnes, and the kit is useful for performing a diagnostic assay. The present cand the kit is useful for performing a diagnostic assay. The present canding frame) contained within the P. acnes polymucleotides of the reading crame) contained within the P. acnes polymucleotides of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly the printed specification, but was obtained in electronic format directly contained within the P. acnes polymetices.

Seguence 88 AA;

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Gaps

0;

Gaps ; Score 39; DB 6; Length 88; Pred. No. 39; 1; Mismatches 2; Indels .. 78.0%; 66.7%; Best Local Similarity 66.7 Matches 6; Conservative Query Match

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5 1 CSVPLTSVC 9 43 CSIPLTKPC g

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AAU43894 standard; protein; 101 AA. RESULT 7 AAU43894

AAU43894;

(first entry) 13-FEB-2002 Propionibacterium acnes immunogenic protein #4790.

SAPHO syndrome; synovitis; acne; pustulosis; hypertosis; osteomyelitis; uveitis; endophthalmitis; bone; joint; central nervous system; ELISA; inflammatory lesion; acne vulgaris; enzyme linked immunosorbent assay; dermatological; osteopathic; neuroprotectant.

Propionibacterium acnes.

WO200181581-A2.

20-APR-2001; 2001WO-US012865

21-APR-2000; 2000US-0199047P. 02-JUN-2000; 2000US-0208841P. 07-JUL-2000; 2000US-0216747P.

Carter D;

Maisonneuve JL; Jones R, Carte

Bhatia A, Benson DR,

CORI-) CORIXA CORP

Bhatia A; Skeiky YAW, Persing DH, Mitcham JL, Wang SS, L'maisonneuve J, Zhang Y, Jen S, Carter D;

WPI; 2001-616774/71. N-PSDB; AAS59521 Propionibacterium acnes polypeptides and nucleic acids useful for vaccinating against and diagnosing infections, especially useful for treating acne vulgaris.

Example 1; SEQ ID NO 5089; 1069pp; English.

us-09-761-636a-10.open.rag

Sequences AAU39105-AAU68017 represent Propionibacterium acnes immunogenic polypeptides. The proteins and their associated DNA sequences are used in the treatment, prevention and diagnosis of medical conditions caused by acnes. The disorders include SAPHO syndrome (synovitis, acne, particularis), uveitis and endophthalmitis.

The disorders include SAPHO syndrome (synovitis, acne, acne, acne, as a series is also involved in infections of bone, joints and the central nervous system, however it is particularly involved in the inflammatory presence or absence of P. acnes in a patient comprises contacting a sample with a binding agent that binds to the proteins of the invention of sample with a binding agent that binds to the proteins of the invention of polypeptides may be used as antigens in the production of antibodies and determining the amount of bound protein in the sample. The copylypeptides may be used as antigens in the production of antibodies of ownregulate expression and activity of P. acnes polypeptides and copyleptides and activity of P. acnes polypeptides an ftp.wipo.int/pub/published_pct_sequences 8\$8888888888888888888888888888888

Sequence 101 AA;

76.0%; Score 38; DB 4; Length 101; 66.7%; Pred. No. 66; 1; Mismatches 1; Indels 6; Conservative |::||| || 16 CNLPLTLVC 24 1 CSVPLTSVC 9 Query Match Best Local Similarity Matches 6; Conserv ð 셤

RESULT 8

ABM40413 standard; protein; 101 AA.

(first entry) 20-OCT-2003 ABM40413;

Propionibacterium acnes predicted ORF-encoded polypeptide #5089. Acne vulgaris; antiseborrhoeic; dermatological; antibacterial; immunostimulant; immune response; vaccine

Propionibacterium acnes

WO2003033515-A1.

24-APR-2003.

11-OCT-2002; 2002WO-US032727.

15-OCT-2001; 2001US-00978825

(CORI-) CORIXA CORP.

Maisonneuve JL; Jones R, Carter D; Bhatía A, Benson DR, Mitcham JL, Skeiky YAW, Persing DH, Zhang Y, Wang S, Jen S, Lodes MJ, Wang S, Jen S, Loge Vallieve-Douglass J; 2003-381789/36. Zhang Y, Barth B,

New Propionibacterium acnes polypeptides and polynucleotides encoding the polypeptide, useful for diagnosing, preventing or treating acne vulgaris, or for stimulating an immune response specific for a P. acnes protein.

N-PSDB; ACF64450.

Example 1; SEQ ID NO 5089; 1481pp; English.

The invention relates to an isolated polynucleotide (ACF64435-ACF64733) encoding a Propionibacterium acnes protein. The invention also relates to polypeptides encoded by the polynucleotides (ABM35624-ABM64536) and to

diditionally encompasses expression vectors and host cells comprising a additionally encompasses expression vectors and host cells comprising a polymucleotide of the invention; antibodies against polypeptides of the invention; duration; fusion proteins comprising a polypeptide of the invention; a zenes method for stimulating an immune response specific for a p. acnes composition comprising T cells prepared to polymucleotides, antibodies, fusion proteins T cell populations, antigen-presenting cells that express the polypeptide); a method and kit for detecting or determining the presence or absence of P. acnes in a patient; and a method for inhibiting the development of P. acnes in a patient; and a method for inhibiting the development of P. acnes in a proteins. T cell populations or antigen-presenting cells that express the compassion of proteins. T cell populations or antigen-presenting cells that express the collypeptides are useful for dagnosing, preventing or treating acnes to protein. The polymucleotides can also be used as probes or primers for uncleic acid hybridisation. The vaccine composition is useful for the stimulation of an immune response against P. acnes, or for treating acnes contained within the P. acnes polymucleotides can also be used as probes or primers for stimulation of an immune response against P. acnes, or for treating acceptance composition is useful for the present contained within the P. acnes polymucleotides of the invention. Note: The sequence data for this patent did not form part of invention. Note: The sequences are for this patent did not form part of the printed specification, but was obtained in electronic format directly and the contained present and presen immunogenic fragments of P. acnes 8888888888888888888888888888888888

Sequence 101 AA;

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Gaps

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Gaps .. DB 6; Length 101; 66; Indels 2; Mismatches Score 38; Pred. No. 76.0%; 6; Conservative Best Local Similarity Query Match Matches

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CNLPLTLVC 24 σ 1 CSVPLTSVC

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RESULT 9 AAU74551

AAU74551 standard; protein; 121 AA.

AAU74551;

08-MAY-2002 (first entry)

Human protein phosphatase 13.31 polypeptide.

WO200212457-A1.

14-FEB-2002.

Mao Y,

Human protein phosphatase 13.31 and encoding polynucleotide, used in diagnosis and treatment of malignant tumors, autoimmune disease and embryonic

Human; protein phosphatase 13.31; enzyme; malignant tumour; cancer; embryonic developmental abnormality; autoimmune disease; antisenescence; gynaecological; cytostatic; immunosuppressant; gene therapy. (BIOW-) BIOWINDOW GENE DEV INC SHANGHAI. development abnormality. Claim 1; Page 30; 34pp; Chinese. 07-JUL-2000; 2000CN-00117017. 02-JUL-2001; 2001WO-CN001118. 2002-172153/22. WPI; 2002-172153/ N-PSDB; ABK14072. Xie Y; Homo sapiens.

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Yue H,
                                                                                                                                                                                                               RESULT 11
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 8266288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention relates to isolated polymucleotide (I) and polypeptide (II) carequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polymucleotides are also used in diagnostics as expressed sequence tags for identifying expressed consistent to the set of the section of (II) is useful in gene therapy techniques to restore normal cativity of (II) or to treat disease states involving (II). (II) is consistent of the sequence tags involving (II). (II) is constituted in thissue, as molecular weight markers and as a food supplement. (II) and its binding pattners are useful in medical imaging of sites expressing (II). (II) and its binding pattners are useful for treating disorders of sites expressing (II). (II) are useful for treating disorders involving aberrant protein expression or biological activity. The colypeptide and polymucleotide sequences have applications in capping it capacities for genetic disorders or other traits to assess blodiversity responsible for genetic disorders or other traits to assess blodiversity amino acid sequences. Abgono10-Abg30377 represent novel human diagnostic amino acid sequences of the invention. Note: The sequence data for this
                                                                                                                                             ö
The invention relates to an isolated polypeptide of human protein phosphatase 13.31 and its associated polynucleotide. The sequences are used in diagnosis and treatment of malignant tumour, embryonic developmental abnormality and autoimmune disease and for studying human antisenescence. This sequence represents human protein phosphatase 13.31
                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
                                                                                                                                                                                                                                                                                                                                                                                        Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder.
                                                                                                                                               ;
                                                                                                                   Length 121;
                                                                                                                                               2; Indels
                                                                                                                   Score 38; DB 5;
Pred. No. 78;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      claim 20; SEQ ID NO 41834; 103pp; English.
                                                                                                                                                                                                                                                                                                                                                                Novel human diagnostic protein #11466.
                                                                                                                                                                                                                                                                             ABG11475 standard; protein; 225 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Tang YT;
                                                                                                                      76.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             30-MAR-2001; 2001WO-US008631.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     31-MAR-2000; 2000US-00540217.
23-AUG-2000; 2000US-00649167.
                                                                                                                                                                                                                                                                                                                                     18-FEB-2002 (first entry)
                                                                                                                                                  6; Conservative
                                                                                                                                                                                                         105 CSVPITDPC 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2001-639362/73.
N-PSDB; AAS75662.
                                                                                                                                                                              1 CSVPLTSVC 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Drmanac RT, Liu C,
                                                                                                                         Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (HYSE-) HYSEQ INC.
                                                                                           Sequence 121 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WO200175067-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              biodiversity.
                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 11-0CT-2001.
                                                                                                                                                                                                                                                                                                            ABG11475;
                                                                                                                                                     Matches
                                                                                                                                                                                                                                                      RESULT 10
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AAF81714 to AAF81740 encode the human proteases and protease inhibitors (PPIMs) given in AAB74668 to AAB74664. The PPIMs can have activities such as: anti-human immunodeficiency virus (HIV); antidiabetic; antithyroid; immunostimulant; immunomodulator; antidiamatory; immunosuppressive; imphrotropic, antigout; thyromimetic; cytostatic; antibacterial; fungicide; protozoacide; antiatreriosclerotic; antiatherosclerotic; virucide; antipsoriatic; and hepatotropic. PPIM polynucleotide and protein sequences can be used in the diagnosis, treatment and prevention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human; protease; protease inhibitor; protease and protease inhibitor; pppM; identification; diagnosis; anti-human immunodeficiency virus; HIV; antidabetic; immunostimulant; immunomodulator; antiinflammatory; antithyroid; immunosuppressive; nephrotropic; antiinflammatory cytostatic; antibacterial; fundicide; protozoacide; antiarteriosclerotic; antiatherosclerotic; antipsoriatic; virucide; hepstotropic; gene therapy; autoimmune disorder; inflammatory disorder; AIDS; DiGeorge's syndrome; severe combined immunodeficiency disease; SCID; Chediak-Higashl syndrome; Crohn's disease; Addison's disease; autoimmune thyroiditis; gout; Crohn's disease; Mabhimoto's thyroiditis; Good pasture's syndrome; infection; Grave's diseases; Hashimoto's thyroiditis; Sjogren's syndrome; cancer; Werner's syndrome; cell proliferative disorder; arteriosclerosis; atherosclerosis;
                                                                                                                                                                                                                                                           0;
patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New protease (inhibitors) useful for diagnosis and treatment of autoimmune/inflammatory disorders such as acquired immunodeficiency syndrome, Cushing's disease, Addison's disease and cell proliferative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Lu DAM;
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                                                                                                                                                                                               Length 225;
                                                                                                                                                                                                                                                              2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Lal P, Tang YT, Bandman O, Baughn MR,
                                                                                                                                                                                                      Score 38; DB 4; I pred. No. 1.4e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human protease and protease inhibitor PPIM-26.
                                                                                                                                                                                                                                                                     1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 1; Page 114-115; 134pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAB74693 standard; protein; 742 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     09-AUG-2000; 2000WO-US021878.
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99US-0160807P.
                                                                                                                                                                                                         76.0%;
66.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
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                                                                                                                                                                               Query Match
Best Local Similarity 66...
6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                  209 ČSVPITDPČ 217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2001-202760/20.
                                                                                                                                                                                                                                                                                                                                       6
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                                                                                                                                              Sequence 225 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WO200110903-A2.
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21-OCT-1999;
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Sun

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AAE01782 standard; protein; 802 AA.
                                                                76.0%; Scor
66.7%; Pred
                                                                                                                                                                                                                                                                12-NOV-1999; 99US-0164744P.
30-JUN-2000; 2000US-0215140P.
                                                                                                                                                                                                                                                       08-NOV-2000; 2000WO-US030628
                                                                                                                                                                                                                                                                             (HUMA-) HUMAN GENOME SCI INC.
                                                                                                                                  (first entry)
                                                                          6; Conservative
                                                                                                                                                                                                                         .802
                                                                                        |}||:|
| CSVPITDPC 734
                                                                                   1 CSVPLTSVC 9
                                                                      Local Similarity
                                                        Seguence 742 AA;
                                                                                                                                                                                                                                      WO200134627-A1
                                                                                                                                  17-JUL-2001
                                                                                                                                                                                                    Homo sapiens.
                                                                                                                                                                                                                                               17-MAY-2001.
                                                                                                                         AAE01782;
                                                                 Query Match
                                                                                           726
                                                                                                                                                                                                                         Protein
                                                                                                                                                                                                                Peptide
                                                                                                       RESULT 12
                                                                                                            AAE01783
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AAD05579-AAD05658 represent cDNAs corresponding to 28 human secreted protein genes and AE01770-AAB01849 represent the proteins they encode. C AAD01850-AAB01860 represent human secreted protein fragments or variants. The genes and their secreted protein are useful for preventing, treating or ameliorating medical conditions, e.g., by protein or gene therapy. The genes and their secreted protein for gene therapy. The genes and their secreted protein or gene therapy. The protein in a sample or by determining the presence of mutations in new protein in a sample or by determining the presence of mutations in the new genes. Specific uses are described for each of the 28 genes, consect on the tissues in which they are most highly expressed, and include disorders, cancer, tumours, foetal and developmental abnormalities, haematopoietic disorders, diseases of the immune system, AIDS, autoimmune of disorders, schizophrenia, asthma, skin disorders (e.g., rheumatoid attricis), inflammation, allergies, autoimmune cognitive disorders, schizophrenia, asthma, skin disorders, and includers, schizophrenia, asthma, skin disorders, cognitive disorders, schizophrenia, asthma, skin disorders, professed, and incleased proteins can also be used to aid wound healing and epithelial cell proliferation, for prevent skin aging due to sunburn, to maintain organs before transplantation, for supporting cell culture of primary tissues, compressive, and in chemotexis, and can be used as a food additive or partners, and in chemotexis, and can be used in alleviating symptoms associated protein of the invention can be used in alleviating symptoms associated radioimmunoassay or enzyme linked immunosorbent assay [ELISA). The reacont seminar animars a human servered enroper enzyme servered enroper enzyme servered enroper enzyments.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               present sequence represents a human secreted protein of the invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 38; DB 4; Length 802;
Pred. No. 5e+02;
1; Mismatches 2; Indels
                                       Claim 11; Page 492-494; 567pp; English.
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66.7%;
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25-APR-2000; 2000US-0199384P.
21-DEC-2000; 2000US-0256931P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              786 CSVPITDPC 794
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 802 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO200177137-A1.
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of autoimmune/inflammatory disorders such as AIDS, DiGeorge's syndrome, severe combined immunodeficiency disease (SCID), Chediak-Higashi syndrome, Cushing's disease, Addison's disease, autoimmune thyroiditis, Crohn's disease, diabetes mellitus, Good parture's syndrome, gout, Grave's disease, Hashimoto's thyroiditis, Sjogren's syndrome, Werner's syndrome, viral, bacterial, fungal, parasitic, protozoal, and helminthic syndrome and cell proliferative disorder such as arteriosclerosis, polymucleotide sequences can be used in somatic or germline gene therapy and in diagnosis of diseases. They can also be used in generating sequences and in molecular biology techniques
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human; secreted protein; proliferative disorder; cancer; tumour; cheatal abnormality; developmental abnormality; haematopoietic disorder; immune system disorder; AlDS; autoimmune disease; rheumatoid arthritis; inflammation; allergy; neurological disorder; Alzheimer* s disease; Parkinson's disease; cognitive disorder; schizophrenia; asthma; skin disorder; psoriasis; sepsis; diabetes; atherosclerosis; cardiovascular disorder; angiogenic disorder; didney disorder; gastrointestinal disorder; angiogenic disorder; didney disorder; endocrine disorder; infection; wound healing; vulnerary; cell culture; chemotaxis; food additive; chromosome 17; binding partner identification.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human gene 13 encoded secreted protein HDPNW93, SEQ ID NO:103.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 742;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /label= Human_mature_secreted_protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 38; DB 4; I
Pred. No. 4.6e+02;
1; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Young PE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1. .19
/label= Signal_peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
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Gaps

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The present invention relates to albumin fusion proteins comprising a therapeutic protein X and human albumin (HA, also known as human serum albumin, HSA). The proteins are useful for treating a disease or disorder that may be modulated by therapeutic protein X. The albumin extends the shelf-life of protein X, and may increase its biological in vitro/in vivo activity. The protein is useful for treating and diagnosing disorders such as cancer, reproductive disorders, disestive disorders (e.g. crohn's disease, ulcerative colitis), immune disorders (e.g. acquired immunodeficiency syndrome, AIDS), endocrine disorders (e.g. diabetes), haematopoietic disorders, neural disorders (e.g. Alzheimer's, parkinson's, Creutzfeldt-Jacob disorders (e.g. Alzheimer's, meningitis, achizophrenia), and comnective disorders (e.g. osteoporosis, arthritis). ABG63326-ABG65518 represent albumin fusion proteins of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      immunosuppressive; antiinflammatory; antiasthmatic; antiallergic; cytostatic; cerebroprotective; neuroprotective; nootropic; cardiovascular; antiatreriosalerotic; gene therapy; human secreted protein; immune disorder; inflammation; respiratory disorder; cancer; CNS disorder; neurodegenerative disorders; inflammatory bowel disease; nephritis; Crohn's disease, asthma; allergy; multiple sclerosis; ischaemic brain injury; Parkinson's disease; Alzheimer's disease, atheroaclerosis; myocarditis; chromosome mapping; triple helix formation; antisense gene therapy; forensic biology.
                                                                                                                       New fusion protein for treating disease e.g. diabetes comprises an albumin fused to a therapeutic protein.
                                                                                                                                                                                 Claim 1; Page 1035-1037; 2102pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADA56848 standard; protein; 802 AA.
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19-JUL-2001; 2001US-0306171P.
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13-NOV-2001; 2001US-0331287P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      76.0%;
             (HUMA.-) HUMAN GENOME SCI INC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         20-NOV-2003 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             6; Conservative
                                                    Rosen CA, Haseltine WA;
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                                                                                       WPI; 2002-010886/01
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 802 AA;
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The invention relates to 592 new human secreted polypeptides useful for diagnosing, treating or preventing e.g. immune disorders, inflammatory conditions, respiratory disorders, cancers, CNS disorders, an included energiative disorders, or polypeptides comprising an amino acid sequence at least 95% identical to the new sequences. The polypeptides, antibodies or antibody fragments that bind to the polypeptides, antibodies or antibody fragments that bind to the polypeptides, antibodies or antibodies, agonists or antagonists that binds to acids encoding the polypeptides, agonists or antagonists that binds to the polypeptide, are useful in preparing diagnostic or pharmaceutical compositions for diagnosing, treating or preventing an e.g. immune compositions for disease), respiratory disorders (e.g. aethma and allergy), cancers (e.g. gastric, ovarian or lung cancer). CNS disorders (e.g. multiple sclerosis or ischaemic Drain injury), neurodegenerative disorders (e.g. parkinson's disease or Alzheimer's disease), and cardiovascular disorders (e.g. atherosclerosis or myocardiits). The cardiovascular disorders (e.g. atherosclerosis or myocardiits). The cardiovascular disorders (e.g. atherosclerosis or myocardiits). The cardiovascular disorders in formation through triple helix formation or antisense DNA or RNA, in gene therapy, for identifying individuals or antisense DNA or RNA, in gene therapy, for identifying individuals or antisense DNA or RNA, in gene therapy, for identifying individuals or proventing neural disorders, information was obtened or reating or preventing neural disorders, infune system disorders, and for treating or preventing neural disorders, incomes sequence corresponds connection of the polypeptide of the invention. Note: The sequence data for this patent did form part of the princed specification, but was obtained in electronic format directly from WIPO at the sequence of t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 wound healing; cytostatic; immunosuppressive; nootropic; neuroprotective; antiviral; antiallergic; heparotropic; antidiabetic; antiinflammatory; vulnerary; cardiant; gene therapy.
                                                       New human secreted polypeptides and polynucleotides, useful for diagnosing, treating or preventing e.g. immune disorders, inflammatory conditions, respiratory disorders, cancers, CNS disorders, or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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                                                                                                                                                                                    Claim 13; SEQ ID NO 1038; 1754pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADA40695 standard; protein; 802 AA.
                                                                                                                                          neurodegenerative disorders.
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786 CSVPITDPC 794
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Best Local Similarity
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                    N-PSDB; ADA55952
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ADA40695
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Score 38; DB 5; Length 802; Pred. No. 5e+02; 1; Mismatches 2; Indels

1; Mismatches

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The invention relates to novel genes ADA3629-ADA40565 and proteins ADA40566-ADA41501 for human secreted proteins, useful for preventing, treating or ameliorating medical conditions e.g. by protein or gene treating or ameliorating medical conditions e.g. by protein or gene fragments, and agonists or antagonists that bind to the polypeptide are diagnostic or preparing a diagnostic or parmaceutical composition for or core treating cancer or other hyperproliferative disorder. The polypeptides and mucleic acid molecules are also useful for detecting, preparing cancer or other hyperproliferative disorders including neoplasms, autoimmune crown them hyperproliferative disorders including neoplasms, autoimmune crown them hyperproliferative disorders (e.g. diabetes, rheumatoid arthritis, systemic lupus canaemia, haematopoietic or haematological disorders (e.g. anaemia, chaematopoietic or haematological disorders (e.g. anaemia, chaematopoietic or haematological disorders (e.g. anaemia, chaematopoietic or parting asthma or eczema, chiflammatory disorders (e.g. ischaemia-reperfusion injury, inflammatory cromporticins adisease), neurodegenerative disorders (e.g. theprendition) and injury, inflammatory disorders of epithelial cell proliferation, radiation hybrid mapping or long-correct of the chromosome identification, radiation hybrid mapping or long-correct or providing immunological probes for differential identification tangent for chromosome immunological probes for differential identification the printed specification but was for correct this patent dinort format directly from MIPO at the printed specification, but was correctly obtained in electronic format directly from WIPO at
                                                                                                                                                                                                                                                                                                                                New human secreted proteins and nucleic acid molecules, useful for preparing a diagnostic or pharmaceutical composition for diagnosing, preventing or treating cancer or other hyperproliferative disorder, asthma, allergies or AIDS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 1; SEQ ID NO 1077; 3205pp; English.
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ftp.wipo.int/pub/published_pct_sequences
                                                                        21-MAR-2001; 2001US-0277340P.
19-JUL-2001; 2001US-0306171P.
13-NOV-2001; 2001US-0331287P.
                          19-MAR-2002; 2002WO-US008123.
                                                                                                                                                                          (HUMA-) HUMAN GENOME SCI INC.
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76.0%; Score 38; DB 6; Length 802; 66.7%; Pred. No. 5e+02; iive 1; Mismatches 2; Indels Query Match 76.0%; Best Local Similarity 66.7%; Matches 6; Conservative Sequence 802 AA;

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. Sequence 10, Application US/09761636A

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Copyright (c) 1993 - 2004 Compugen Ltd.
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ALIGNMENTS

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Gaps
APPLICANT: ACHEN, Marc

APPLICANT: STACKER, Steven

APPLICANT: STACKER, Steven

APPLICANT: STACKER, Richard

APPLICANT: STACKER, Richard

APPLICANT: CENDRON, Angela

TITLE OF INVENTION: VEGP-D/VEGF-C/VEGF PEPTIDOMIMETIC INHIBITOR
FILE REPERENCE: 1064/48505 Achen et al

CURRENT FILING DATE: 2001-01-18

PRIOR APPLICATION NUMBER: US 60/176,293

PRIOR PLING DATE: 2000-01-18

PRIOR PLING DATE: 2000-01-18

PRIOR FILING DATE: 2000-05-16

NUMBER OF SEQ ID NOS: 34

SQFTWARE: Patentin version 3.0

LENGTH: 9

***CHART OF THE CONTROL OF 
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tive 0; Mismatches 0;
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Matches 9, Conservative
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; ORGANISM: Homo sapiens
US-09-761-636A-10
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Sequence 174316, Application US/10424599
; Sequence 174316, Application US/10424599
; Publication No. US20040031072A1
; GRNERAL INFORMATION:
; APPLICANT: Kovalic David K
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21 (5323) B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 174316
; LENGTH: 359
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APPLICANT: La Rosa Thomas J
APPLICANT: Avair David K
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
TITLE OF INVENTION NUMBER: US/10/424,599
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 205890
TYPE: PRT
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55;
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Pred. No. 13;
2; Mismatches 1; Indels
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                                                                                                                                                             ; OTHER INFORMATION: Clone ID: PAT_MRT3847_28570C.1.pep
US-10-424-599-206581
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OTHER INFORMATION: unsure at all Xaa locations
FRATURE:
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NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 206581
LENGTH: 78
                                                                                                                                                                                                                                       82.0%;
66.7%;
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Best Local Similarity 66.7
Matches 6; Conservative
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                                                                                                            TYPE: PRT
ORGANISM: Glycine max
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US-10-424-599-205890
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Publication No. US20040031072A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT:
APPLICANT:
APPLICANT:
Cao Yongwei
TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
FILE REFREENCE:
S18-21(53223)B
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US-10-424-599-241616
Sequence 241616, Application US/10424599
Publication No. US20040031072A1
Sequence 241616, Application US/2040031072A1
Sequence 241616, Application No. US20040031072A1
SERICANT: La Rosa Thomas J
APPLICANT: Zhou Yihua
APPLICANT: Zhou Yihua
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Uses Thereof for Plant Improvement
FILE REFRENCE: 38-21(53223)B
CURRENT REPLIANG DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
                                           APPLICANT: La Rosa Thomas J
APPLICANT: La Rosa Thomas J
APPLICANT: En Rosa Thomas J
APPLICANT: Avalic David K
APPLICANT: Avalic David K
APPLICANT: Covalic David K
APPLICANT: Cao Yougwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REPRENCE: 38-21 (53223) B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 241613
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 154;
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; OTHER INFORMATION: Clone ID: PAT_MRT3847_60206C.1.pep
US-10-424-599-241616
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US-10-424-599-241613
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 42; DB
Pred. No. 16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   84.0%;
77.8%;
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Best Local Similarity 77.8
Matches 7; Conservative
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ORGANISM: Glycine max
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                            GENERAL INFORMATION:
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LENGTH: 194
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Sequence 1081, Application US/10369493

Sequence 1081, Application US/20030233675A1

Sequence 1081, Application No. US20030233675A1

GENERAL INPORMATION:

APPLICANT: Slater, Steven C.

APPLICANT: Gladman, Barry S.

APPLICANT: Goldman, Barry S.

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                                                                                                                                                         Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 276101, Application US/10424599
Publication No. US20040031072A1
GENERAL INFORMATION:
APPLICANT: La Rosa Thomas J
APPLICANT: Zhou Yihua
APPLICANT: And Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
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                                                                                      Score 41; DB 16; Length 883;
Pred. No. 1.3e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 39; DB 12; Length 63;
Pred. No. 23;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; OTHER INFORMATION: Clone ID: PAT_MRT3847_91339C.1.pep
US-10-424-599-276101
                                                                                                                                               0; Mismatches
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CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
LENGTH: 63
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                                                                                  82.0%;
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66.7%;
                                                                                                                                                  Conservative
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Matches 7; Conservative
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                                                                                                                                                                                                         1 CSVPLTSV 8
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                                                                         Query Match
Best Local Similarity
Matches 8; Conserv
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Best Local Similarity
                      US-10-437-963-133870
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US-10-369-493-1081
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APPLICANT: Li, Ping
TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21 (5321)B
CURRENT APPLICATION NUMBER: US/10/437,963
CURRENT FILING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Zhou, Yihua
APPLICANT: Zhou, Yihua
APPLICANT: Kevalic, David K.
APPLICANT: Streen, Steven E
APPLICANT: Tabaska, Jack E
APPLICANT: Tabaska, Jack E
APPLICANT: Tabaska, Jack E
APPLICANT: Tabaska, Jack E
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53313) B
CURRENT APPLICATION NUMBER: US/10/425,114
NUMBER OF SEQ ID NOS: 73128
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Pred. No. 82;
2; Mismatches 1; Indels
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                         FEATURE:

CTHER INFORMATION: Clone ID: PAT_MRT3847_27947C.1.pep

US-10-424-599-205890
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US-10-425-114-69391
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Publication No. US20040123343A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 69391, Application US/10425114
Publication No. US20040034888A1
GENERAL INFORMATION:
APPLICANT: Liu, Jingdong
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Wu, Wei
APPLICANT: Wu, Wei
APPLICANT: Boukharov, Andrey A.
APPLICANT: Barbazuk, Brad
                                                                                                                                                      Query Match
Best Local Similarity 66.7%;
Matches 6; Conservative
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Best Local Similarity 66.74
The Grandstreen of Conservative
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82 CSSPITSIC 90
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ORGANISM: Glycine max
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ORGANISM: Glycine max
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APPLICANT: La Rosa Thomas J

APPLICANT: La Rosa Thomas J

APPLICANT: Kovalic David K

APPLICANT: Zhou Yihua

APPLICANT: Zhou Yihua

APPLICANT: CANT: CAN YONGWei

TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With

TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

FILE REFERENCE: 38-21(5323)B

CURRENT APPLICATION WNDER: US/10/424,599

CURRENT PILING DATE: 2003-04-28

NUMBER OF SEQ ID NOS: 285684

SEQ ID NO 276082

TVDF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 243236, Application US/10424599
; Sequence 243236, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21 (53223) B
CURRENT FILING DATE: 2003-04-28
; UWRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 24326
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US-10-424-599-243236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OTHER INFORMATION: Clone ID: PAT_MRT3847_91321C.1.pep
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  74.0%; Score 37; DB 12;
55.6%; Pred. No. 1.3e+02;
iive 1; Mismatches 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           74.0%; Score 37; DB 12; 66.7%; Pred. No. 73;
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OTHER INFORMATION: unsure at all Xaa locations
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 56269, Application US/10425114; Publication No. US20040034888A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Liu, Jingdong
APPLICANT: Zhou, Yihua
APPLICANT: Kovalic, David K.
PRELICANT: Screen, Steven E
APPLICANT: Tabaska, Jack E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 74.0
Best Local Similarity 55.6
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity 66.7
Matches 6; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 CSVPLTSVC 9
                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT
ORGANISM: Glycine max
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 CSVPOTGLC
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US-10-424-599-243236
                                                                                                                                                                                                                                                                                                                                                                                                                                    FEATURE:
NAME/KEY: unsure
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Sequence 169061. Application US/10424599
Sequence 169061. Application US/10424599
Publication No. US20040031072A1
GENERAL INFORMATION:
APPLICANT: La Rosa Thomas J
APPLICANT: Zhou Yihua
APPLICANT: Zhou Yihua
APPLICANT: Zou Yongwei
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFRENCE: 38-21(5323.8
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
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Pred. No. 3.9e+02;
1; Mismatches 2; Indels
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                                                                                                                                                                                                                                                Sequence 888, Application US/0983245;
Publication No. US20040010134A1
GENERAL INFORMATION:
APPLICANT HUMAN GENOME Sciences, Inc.
TITLE OF INVENTION: Albumin Fusion Proteins
FILE REPRENCE: PF946CT
CURRENT APPLICATION NUMBER: US/09/833,245
CURRENT FILING DATE: 2001-04-12
PRIOR APPLICATION NUMBER: 60/229, 358
PRIOR FILING DATE: 2000-04-12
PRIOR FILING DATE: 2000-04-12
PRIOR APPLICATION NUMBER: 60/199, 384
PRIOR FILING DATE: 2000-04-25
NUMBER OF SEQ ID NOS: 2267
SOFTWARE: PALENTIN VET. 2.1
SEQ ID NO 988
LENGTH: 802
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Similarity 66.7%;
6; Conservative 1
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786 CSVPITDPC 794
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 CSVPLTSVC 9
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Best Local Similarity
Matches 6; Conserv
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LENGTH: 82
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US-09-833-245-888
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## APPLICANT: Cao, Yongwei

TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REPERBENCE: 38-21(53313)8

CURRENT APPLICATION NUMBER: US/10/425,114

CURRENT FILING DATE: 2003-04-28

NUMBER OF SEQ ID NOS: 73128

SEQ ID NO 56269

LENGTH: 215

TYPE: PRT

ORGANISM: Glycine max

FERTURE:

ORGANISM: Glycine max

FERTURE:

ORTHER INFORMATION: Clone ID: 700835470_FLI.pep
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183 CSPPLTATC 191
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Query Match
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Sequence 10842, A
Sequence 20364, A
Sequence 1, Appli
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Sequence 4, Appli
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Sequence 51, Appl
Sequence 51, Appl
Sequence 51, Appl
Sequence 51, Appl
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Sequence 3, Appli
Sequence 3, Appli
                                                                     5, 2004, 09:55:30; Search time 8 Seconds (without alignments) 58.079 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
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(cgn2_6/ptodata/2/iaa/5A_COMB.pep:*
(cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
(cgn2_6/ptodata/2/iaa/6A_COMB.pep:*
(cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
(cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
(cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
(cgn2_6/ptodata/2/iaa/backfiles1.pep:*
    GenCore version 5.1.6
(c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-08-840-062-7

US-09-252-991A-20364

US-08-688-342-1

US-09-113-788-1

US-09-113-788-1

US-09-113-788-1

US-09-113-788-1

US-09-61-976-4725

US-09-134-012-3

US-09-673-395A-479

US-09-673-395A-479

US-09-673-395A-479

US-09-673-395A-479

US-09-673-391A-479

US-09-673-391A-479

US-09-673-391A-479

US-09-673-391A-6083

US-09-496-672-51

US-09-496-672-51

US-09-496-188-1

US-09-469-188-1

US-09-469-188-1

US-09-469-188-1

US-09-252-991A-26927

US-08-431-246B-24

US-08-533-246B-24
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US-09-489-039A-13837
US-09-252-0013
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US-09-252-991A-30882
                                                                                                                                                                                                                      Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                   389414 seqs, 51625971 residues
                                                                                                                                                                                                                                                                               Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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seq length: 200000000
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Match Length
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28 32 64.0 323 3 0.0 60-315-35-9 Sequence 9, Appl. 32 64.0 353 3 US-06-315-795-9 Sequence 9, Appl. 32 64.0 353 4 US-06-345-795-3 Sequence 17, Appl. 32 64.0 353 4 US-06-345-795-3 Sequence 17, Appl. 32 64.0 353 4 US-06-345-795-3 Sequence 18, Appl. 32 64.0 353 4 US-06-345-795-3 Sequence 18, Appl. 32 64.0 352 4 US-06-35-795-3 Sequence 18, Appl. 32 64.0 10.0 4 US-06-360-359-9 Sequence 18, Appl. 32 64.0 10.0 4 US-06-397-631-15 Sequence 18, Appl. 32 64.0 110.0 4 US-06-397-631-15 Sequence 5, Appl. 42 31 62.0 14 2 US-06-397-631-5 Sequence 5, Appl. 42 31 62.0 14 2 US-06-397-631-5 Sequence 5, Appl. 42 31 62.0 14 4 US-06-397-631-5 Sequence 5, Appl. 43 10.50-397-85-5 Sequence 5, Appl. 44 3 US-06-397-935-5 Sequence 5, Appl. 45 31 62.0 14 5 PC-1639-08326-5 Sequence 5, Appl. 44 3 US-06-397-935-5 Sequence 5, Appl. 45 31 62.0 14 5 PC-1639-08326-5 Sequence 5, Appl. 45 Sequence 7, Appl. 44 US-06-397-935-5 Sequence 5, Appl. 45 Sequence 7, Appl. 44 US-06-397-935-5 Sequence 5, Appl. 45 Sequence 7, Appl. 44 US-06-397-935-5 Sequence 5, Appl. 45 Sequence 7, Appl. 44 US-06-397-935-5 Sequence 5, Appl. 45 Sequence 7, Appl. 44 US-06-397-935-5 Sequence 5, Appl. 45 Sequence 7, Appl. 44 US-06-397-935-5 Sequence 5, Appl. 45 Sequence 6, Appl. 45 Sequence 7, Appl. 45 Sequence 7, Appl. 45 Sequence 7, Appl. 45 Sequence 7, Appl. 45 Sequence 6, Appl. 45 Sequence 7, Appl. 45 Sequence 6, Appl. 45 Sequence 7, Appl. 45 Sequence 8, Appl. 45 Sequence 8, Appl. 45 Sequence 8, Appl. 45
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Gaps
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APPLICANT: Au-Young, Janice
APPLICANT: Cocks, Benjamin G.
APPLICANT: Goli, Surya K.
APPLICANT: Hillman, Jennifer L.
TITLE OF INVENTION: NOVEL HUMAN C-TYPE LECTIN
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Forter Drive
CITY: Palo Alto
                                                                                                                                                                                                                                   OPERATING SYSTEM: DOS.
SOFTWARE: FastSEQ Version 1.5
CURRENT APPLICATION DATA:
ATPLICATION NUMBER: US/08/68,342
FILING DATE: Filed Herewith
ATTORNEY/ABORT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0095-1 CIP
TELECOMMUNICATION INFORMATION:
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APPLICATION NUMBER: 08/688,342
FILING DATE:
ATTORNEY AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 1, Application US/09113788 Patent No. 5969104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: 415-845-4166
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                       MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DENGTH: 201 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
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Best Local Similarity 66.7
Matches 6; Conservative
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                                                                                                                                         COMPUTER READABLE FORM:
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Palo Alto
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                                                                                                    94304
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-08-688-342-1
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                                                                      COUNTRY:
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APPLICANT: Marc J. Rubenfield et al.

APPLICANT: Marc J. Rubenfield et al.

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS

TITLE OF INVENTION: AERUGINCAS FOR DIAGNOSTICS AND THERAPEUTICS

TITLE OF INVENTION: AERUGINCAS FOR DIAGNOSTICS AND THERAPEUTICS

FILE REFERENCE: 107196.136

CURRENT PELING DATE: 1999-02-18

PRIOR FILING DATE: 1999-02-18

PRIOR FILING DATE: 1998-02-18

PRIOR FILING DATE: 1998-02-18

PRIOR FILING DATE: 1998-02-18

PRIOR FILING DATE: 1998-02-18

SEQ ID NOS: 33142

LENGTH: 168
                                                                                                        GENERAL INFORMATION:

APPLICANT: GATYONS

APPLICANT: GATY Breton et. al

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA

TITLE OF INVENTION: NUCLEIC ACID AND THERAPEUTICS

FILE REFERENCE: 2709,2004001

CURRENT PAPPLICATION NUMBER: US/09/489,039A

CURRENT FILING DATE: 2000-01-27

PRIOR APPLICATION NUMBER: US 60/117,747

PRIOR APPLICATION NUMBER: 1999-01-29

NUMBER OF SEQ ID NOS: 14342

SEQ ID NO 10842
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Pred. No. 52;
0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  82.0%; Score 41; DB 4; Length 422; 100.0%; Pred. No. 19; ive 0; Mismatches 0; Indels
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Patent No. 581264
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Au-Young, Janice
APPLICANT: Gocks, Benjamin G.
APPLICANT: Hillman, Jennifer L.
TITLE OF INVENTION: NOVEL HUMAN C-TYPE LECTIN
NUMBER OF SEQUENCES: 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
                                        Sequence 10842, Application US/09489039A Patent No. 6610836
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-20364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Klebsiella pneumoniae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 66.7%;
Matches 6; Conservative
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Best Local Similarity 100.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    387 SVPLTSVC 394
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                  US-09-489-039A-10842
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US-08-688-342-1
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us-09-761-636a-10.open.rai

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APPLICANT: Abramovitz, Mark
APPLICANT: Boie, Yves
APPLICANT: Brie, Yves
APPLICANT: Grygor-zyk, Richard
APPLICANT: Metters, Kathleen
APPLICANT: Rushmore, Thomas H.
APPLICANT: Slipetz, Deborah M.
TITLE OF INVENTION: DNA ENCODING PROSTAGLANDIN RECEPTOR IP
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 34; DB 4; Length 134;
Pred. No. 90;
1; Mismatches 3; Indels
                                                                                                                                                         Sequence 4725, Application US/09621976
Fatent No. 6639063
GENERAL INFORMATION:
APPLICANT: Dumas Milne Edwards, J.B.
APPLICANT: Johert, S.
APPLICANT: Johert, S.
APPLICANT: Glordano, J.Y.
ITLE OF INVENTION: ESTE and Encoded Human Proteins.
FILE REFERENCE: GENSET 054PR2
CURRENT APPLICANTION NUMBER: US/09/621,976
CURRENT FILING DATE: 2000-07-21
NUMBER: OF SEQ ID NOS: 19335
SEQ ID NO 4725
LENGTH: 134

LENGTH: 134
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US-08-134-012-3
Sequence 3, Application US/08134012
Patent No. 5516652
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         E: John Wallen
126 E. Lincoln Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LOCATION: 49,51
OTHER INFORMATION: Xaa = Ala,Gly
NAME/KEY: UNSURE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LOCATION: 44
OTHER INFORMATION: Xaa = Cys, Trp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LOCATION: 47
OTHER INFORMATION: Xaa = Gly, Arg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OTHER INFORMATION: Xaa = Lys, Arg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; LOCATION: 45
; OTHER INFORMATION: Xaa = Phe, Leu
US-09-621-976-4725
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55.6%;
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OTHER INFORMATION: Xaa =
NAME/KEY: UNSURE
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                                            293 CSIPIWKIC 301
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                   1 CSVPLTSVC 9
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STATE: New Jersey
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
Matches 5; Conserv
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US-08-586-165-4
Sequence 4, Application US/08586165
Patent No. 6054298
GENERAL INFORMATION:
APPLICANT: Laufer, Edward M.
APPLICANT: Tabin, Clifford J.
TITLE OF INVENTION: Fringe Proteins and Pattern Formation VOMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
                                                                                                                                                                                                                                                                                                          Query Match 72.0%; Score 36; DB 2; Length 201; Best Local Similarity 66.7%; Pred. No. 63; Matches 6; Conservative 1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 359;
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44.4%; Pred. No. 1.6e+02;
tive 3; Mismatches 2; Indels
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MEDIUM TYPE: Floppy disk
COMPUTER: Elem PC compatible
COMPUTER: Ploppy disk
COMPUTER: PLOPS MS-DOS
COMPUTER: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/586,165
FILING DATE: 16-JAN-1996
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Granahan, Patricia
REGISTRATION NUMBER: 32.227
REFERENCE/DOCKET NUMBER: HU95-05
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 861-6240
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE GRARACTERISTICS:
LENGTH: 359 amino acids
TYPE: amino acid
STRANDEDDESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            E: Hamilton, Brook, Smith & Reynolds, Two Militia Drive
                                      TELEFAX: 415.845-4166
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHRACTERISTICS:
LENGTH: 201 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
TELECOMMUNICATION INFORMATION: TELEPHONE: 415-855-0555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STREET: Two Millian or
CITY: Lexington
STATE: Massachusetts
COUNTRY: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity 44.4
Matches 4; Conservative
                                                                                                                                                                                 MOLECULE TYPE: peptide IMMEDIATE SOURCE: LIBRARY: MMLRIDT01 CLONE: 515847
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                  187 CSVPSYSIC 195
                                                                                                                                                                                                                                                                                                                                                                                              1 CSVPLTSVC 9
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LOCATION: 1..1
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Gaps
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; Patent NO. 6365360
; GENERAL INFORMATION:
; APPLICANT: Abramovitz, Mark
APPLICANT: Grygorczyk, Richard
APPLICANT: Methers, Kathleen
APPLICANT: Methers, Kathleen
APPLICANT: Ribpetz, Deborah M.
APPLICANT: Slipetz, APPLICANT: Slipetz, Deborah M.
APPLICANT: Slipetz, APPLICANT: Slipetz, Deborah M.
APPLICANT: Slipetz, Slipetz, Deborah M.
APPLICANT: Slipetz, APPLICANT: Slipetz, Deborah M.
APPLICANT: Slipetz, APPLICANT: Slipetz
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                                                                                                                                                                                                                Length 386;
                                                                                                                                                                                                           Query Match 68.0%; Score 34; DB 1; Length 386 Best Local Similarity 66.7%; Pred. No. 2.6e+02; Matches 6; Conservative 1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CITY: Rahway
STATE: New Jersey
COUNTRY: USA
ZIP: 07065-0907
COMPUTER READABLE FORM:
MEDIUM TWEE Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: BE PC compatible
COMPUTER: BE PC compatible
COMPUTER: BE PC COMPATIBLE
SPECIATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/039,798
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/520,519
FILING DATE: 29-AUG-195
ATTORNEY/AGENT INFORMATION:
NAME: Hand, J. Mark
REGISTRATION NUMBER: 36,545
REFERENCE/DOCKET NUMBER: 19098DB
TELECOMMUNICATION:
TELEPHONE: (732) 594-3905
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; Sequence 479, Application US/09673395A
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INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 386 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; TOPOLOGY: linear; MOLECULE TYPE: protein US-09-039-798-3
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251 CSLPLTIRC 259
                                                                     MOLECULE TYPE: protein US-08-520-519-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       251 CSLPLTIRC 259
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E: New Jersey
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                          TOPOLOGY: linear
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US-09-673-395A-479
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US-09-039-798-3
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APPLICANT: Boie, Yves
APPLICANT: Boie, Yves
APPLICANT: Boie, Yves
APPLICANT: Grygorczyk, Richard
APPLICANT: Metters, Kathleen
APPLICANT: Rushmore, Thomas H.
APPLICAN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VERMINING SIGLEM:
VERMINING SIGLEM:
VERMINING SIGLEM:
VERMINING SIGNATION DATA:
APPLICATION NUMBER:
FILING DATE:
FILING DATE: 29-40G-1995
CLASSIFICATION:
SIGNATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Tribble, Jack L.
REGISTRATION NUMBER: 32,633
REFERENCE/DOCKET NUMBER: 19098DA
TELECOMMUNICATION INFORMATION:
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CITY: Rahway
STATE: New Jersey
COUNTRY: USA
ZIP: 07065-0907
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
C
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; Sequence 3, Application US/08520519
; Patent No. 5728808
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEPHONE: (908) 594-5321 INFORMATION FOR SEQ ID NO: 3: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 386 amino acids
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Best Local Similarity 66.7;
Matches 6; Conservative
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MOLECULE TYPE: protein
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US-08-134-012-3
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68.0%; Score 34; DB 3; Length 747; 66.7%; Pred. No. 5.1e+02; tive 0; Mismatches 3; Indels
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GENERAL NO. 6219429;
GENERAL THYORMATION:
APPLICANT: Takahashi, Joseph S.
APPLICANT: Turek, Fred W.
TITLE OF INVENTION: CLCCK GENE AND GENE PRODUCT
FILE REFERENCE: 0290-5
CURRENT APPLICATION NUMBER: 08/9496,672
CURRENT FILING DATE: 1997-06-30
PRIOR PILING DATE: 1997-06-30
PRIOR FILING DATE: 1997-06-30
PRIOR FILING DATE: 1997-06-30
PRIOR FILING DATE: 1997-06-30
SEQ ID NO 550
SEQ ID NO 51

LENGTH: 747
                                                                                                                                                                                             APPLICANT: Takanshi, Joseph S.
APPLICANT: Takanshi, Joseph S.
APPLICANT: Turek, Fred W.
APPLICANT: Turek, Fred W.
TITLE OF INVENTION: CLOCK GENE AND GENE PRODUCT
FILE REFERENCE: 0290-5
CURRENT APPLICATION NUMBER: US/08/885,291A
CURRENT APPLICATION NUMBER: 08/816,693
EARLIER APPLICATION NUMBER: 08/816,693
EARLIER FILING DATE: 1997-03-13
NUMBER OF SEQ ID NOS: 55
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 51
LENGTH: 747
                                                                                                                             US-08-885-291-51; Sequence 51, Application US/08885291A; Patent No. 6057125; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 51, Application US/09496672
Patent No. 6291429
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US-09-402-016A-4
; Sequence 4, Application US/09402016A
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Best Local Similarity 66.7
Matches 6; Conservative
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Best Local Similarity 66.7
Matches 6; Conservative
                                                          215 CRVPLGKVC 223
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                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT; ORGANISM: Mus musculus
US-08-885-291-51
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                        CSVPLTSVC 9
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GENERAL INFORMATION:
APPLICANT: SPECHT, THOMAS
APPLICANT: HINZMANN, BERND
APPLICANT: HINZMANN, BERND
APPLICANT: PILARSKY, CHRISTIAN
APPLICANT: PILARSKY, CHRISTIAN
APPLICANT: PILARSKY, CHRISTIAN
APPLICANT: PILARSKY, CHRISTIAN
APPLICANT: BOGAR
APPLICANT: BOGAR
APPLICANT: BOGAR
APPLICANT: BOGAR
CURRENT ROSENHHAL, ANDRE
CURRENT APPLICATION NUMBER: US/09/673,395A
CURRENT FILING DATE: 2000-10-17
SEQ ID NO 479
LENGTH: 400
LENGTH: 400
LENGTH: 400
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                                                                                                                                                                                                                                                                                                                                                                                             0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 51, Application US/08816693A; Patent No. 5874241; Patent No. 5874241; RENERAL INFORMATION:
APPLICANT: Takahashi, Joseph S; APPLICANT: Turek, Fred W
TITLE OF INVENTION: Clock Gene and Gene Product NUMBER OF SEQUENCES: 53
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dressler, Rockey, Milnamow & Katz STREET: Two Prudential Plaza, Suite 4700
                                                                                                                                                                                                                                                                                                                                                                                          1; Mismatches
                                                                                                                                                                                                                                                                                                                                                  Query Match 68.0 Best Local Similarity 85.7 Matches 6; Conservative
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STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: linear MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                               ; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-673-395A-479
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STREET: Two Pruder CITY: Chicago STATE: Illinois COUNTRY: USA ZIP: 60601
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Best Local Similarity
Matches 6; Conserv
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US-08-816-693A-51
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Best Local Similarity 85.7%; Pred. No. 1.2e+02;
Matches 6; Conservative 0; Mismatches 1; Indels
                                                                                                                                                       Search completed: September 5, 2004, 10:21:59 Job time: 9 secs
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5, 2004, 09:47:29; Search time 5.37374 Seconds (without alignments) 125.302 Million cell updates/sec
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                           OM protein - protein search, using sw model
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42
                                                                                                                          September
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Run on:

283366 seqs, 96191526 residues BLOSUM62 Gapop 10.0 , Gapext 0.5 1 CVPLTSC 7 Perfect score: Scoring table: Sequence: Searched: Title:

283366 Total number of hits satisfying chosen parameters:

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries seq length: 0 seq length: 200000000 Minimum DB Maximum DB

1: pirl:* 2: pir2:* 3: pir3:* 4: pir4:* 78:* PIR Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Description	suface antigen - p retrovirus-related cellodextrin phosp alpha-51D immobili alpha-51D immobili integumentary muci mucin 2, intestina zonadhesin - pig protein kinas Akz keratin KAPS.4 - s hypothetical prote hypothetical prote ultra-high-sulfur gene 20 protein - hypothetical prote hypothetical prote hypothetical prote hypothetical prote protein M28.1 [imp E20D23.20 protein hypothetical prote mucin 2 precursor, hemocytin - silkwo proteinase inhibit hypothetical prote mucin 2 precursor, hemocytin - silkwo proteinase inhibit hypothetical prote hypothetical prote proteinase inhibit hypothetical prote hypothetical prote proteinase inhibit hypothetical prote hypothetical prote proxisome assembl	
Ω	T31687 1731687 170045 T700045 T700045 T700045 T728674 T30886 A554895 S66336 S66336 S66336 S6334 S73374 C33374 C33374 C33374 C41233 F82297 T42990 T42990 T42933 B5712 F84712	
DB		
Length	2533 2533 2533 2533 2533 2533 2533 2007 207 207 207 208 208 209 209 303 303 3133 3133 3133 3133 3133 3133	
% Query Match	99279 88577 88574 88574 8810 9810 7886 7886 7886 7886 7886 7886 7886 788	
Score	 	
Result No.	I	

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16	16	16	26	76.2	26	76	73	73	73	73	73	73	73	73	73
32	32	32	32	32	32	32	31	31	31	31	31	31	31	31	31
30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

RESULT 1

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		ar-2001		family i							0; Gaps
		3-Ma		ans							.;
	suface antigen - Paramecium primaurelia C;Species: Paramecium primaurelia	C;Date: 19-May-2000 #sequence_revision 19-May-2000 #text_change 23-Mar-2001 C;Accession: T31687	R;Bourgain-Guglielmetti, F.; Caron, F. Journal of Bukaryot. Microbiol. 43, 303-314. 1996	A.Title: Molecular characterization of the D surface protein gene subfamily in A.Reference number: Z21061; MUID:96313351; PWID.8758414	31687 iminary	e: DNA 2543 <boii></boii>	A:Cross_references: EMBL:X96616; NID:g1235576; PIDN:CAA65436.1 C:Genetics:	: SGC5	C;Superfamily: G surface protein	Query Match 92.9%; Score 39; DB 2; Length 2543; Best Local Similarity 71.4%; Pred. No. 26.	0; Indels
T31687	suface antiger C;Species: Par	C; Date: 19-May-2000 C; Accession: T31687	R;Bourgain-Guc Journal of Euk	A; Title: Molec A; Reference nu	A;Accession: T31687 A;Status: preliminary	A; Molecule type: DNA A; Residues: 1-2543 < BOUS	A; Cross-refere	A, Genetic code: SGC5	C;Superfamily:	Query Match Best Local S	Matches 5

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RESULT

0

Gaps

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Indels

Length 2533;

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integumentary mucin B.1 - African clawed frog (fragment)

(;Species: Xenopus laevis (African clawed frog)

(;Species: Xenopus laevis (African clawed frog)

(;Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 03-Nov-2000

(;Date: 21-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 03-Nov-2000

(;Accession: T30886

A;Title: Similarities of integumentary mucin B.1 (FIM-B.1) from Xenopus laevis and prep A;Reference number: 220920; MUID:97153143; PMID:8998664

A;Reference number: Z20920; MUID:97153143; PMID:8998664

A;Reference number: D15086

A;Reference number: D15086

A;Residues: preliminary; translated from GB/EMBL/DDBJ

A;Residues: preliminary; translated from GB/EMBL/DDBJ
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R;Ohmori, H.; Dohrman, A.F.; Gallup, M.; Tsuda, T.; Kai, H.; Gum Jr., J.R.; Kim, Y.S.; J. Biol. Chem. 269, 17833-17840, 1994
A;Title: Molecular cloning of the amino-terminal region of a rat MUC 2 mucin gene homol A;Reference number: A54895; MUID:94299489; PMID:8027037
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A, Accession: A54895
A; Status: preliminary
A; Molecule type: mRNA
A; Molecule type: mRNA
A; Residues: 1-1513 < 0HM>
A; Cross-references: GB:U07615
C; Superfamily: von Willebrand factor; von Willebrand factor type A repeat homology; vo
C; Keywords: intestine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Cross-references: EMBL: Y08296; NID: 91839051; PIDN: CAA69604.1; PID: 91839052
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            mucin 2, intestinal/tracheal - rat (fragment)
C;Species: Rattus norvegicus (Norway rat)
C;Date: 23-Mar-1995 #sequence_revision 23-Mar-1995 #text_change 11-Jan-2000
                                                                                                                                                                                                                                                     A;Cross-references: EMBL:X85135; NID:g728634; PID:g728635; PIDN:CAA59447.1 C;Genetics: BGC5 Squetic code: SGC5 A;Note: alpha-51D C;Superfamily: G surface protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   81.0%; Score 34; DB 2; Length 151
71.4%; Pred. No. 1.5e+02;
ive 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           81.0%; Score 34; DB 2; I
71.4%; Pred. No. 1.5e+02;
cive 1; Mismatches 1;
                                                                                      A;Reference number: 220505
A;Accession: T28674
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-2533 <SCH>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  85.7%; Score 36; DB 2;
57.1%; Pred. No. 98;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3; Mismatches
                                    R;Schmidt, H.J. submitted to the EMBL Data Library, March 1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C; Superfamily: pig submaxillary mucin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
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Best Local Similarity 71.4
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4; Conservative
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2149 CIPITNC 2155
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Best Local Similarity
Matches 5; Conserv
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Best Local Similarity
Matches 4; Conserv
C; Accession: T28674
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                                                                                                                                                                                                                                                                                                                                                                                                                                          Cispecies: Clostridium thermocellum cospecies: Clostridium thermocellum cospecies: Clostridium thermocellum cospecies: Clostridium thermocellum cospecies: 22-Jan-1999 #sequence_revision 22-Jan-1999 #text_change 15-Oct-1999 CiAccession: T00649 #sequence_revision 22-Jan-1999 #text_change 15-Oct-1999 CiAccession: T00645 Tikeschi, Y.; Tsutsumi, N.; Kan, A.; Sumitani, J.; Arai, M. S.; Kawaguchi, T.; Ikeuchi, Y.; Tsutsumi, N.; Kan, A.; Sumitani, J.; Arai, M. A.; Ferment. Bloeng. 85, 144-149, 1998 A; Fittle: Cloning, nucleotide sequence, and expression of the Clostridium thermocellum ce A; Accession: T00045 A; Accession: T00045 A; Cross prefiminary; translated from GB/EMBL/DDBJ A; Residues: 1-980 cKAW> A; Residues: 1-980 cKAW> A; Residues: 1-980 cKAW> A; Cross references: EMBL:AB006822; NID:d1117395; PIDN:BAA22081.1; PID:d1022940 A; Experimental source: ATCC 27405 C; Genetics: A; Genetics: A; Genetics: Cigmetics: Cigm
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C;Species: Paramecium tetraurelia
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 17-Mar-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         alpha-51D immobilization antigen - Paramecium tetraurelia
C;Species: Paramecium tetraurelia
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 20-Jun-2000
C;Accession: T28675
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85.7%; Score 36; DB 2; Length 2533;

Best Local Similarity 57.1%; Pred. No. 98;

Matches 4; Conservative 3; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 36; DB 2; Length 980;
Pred. No. 44;
3; Mismatches 0; Indels
                                                                               Length 380;
                                                                                                                                                       0; Indels
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submitted to the EMBL Data Library, March 1996
A;Reference number: 220506
A;Accession: T28675
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Rolecule type: DNA
A;Residues: 1-2333 s.CH>
A;Residues: 1-2333 s.CH>
A;Cross-references: EMBL:X96400; PIDN:CAA65264.1
                                                                                      DB 2;
                                                                           Query Match
90.5%; Score 38; DB 2
Best Local Similarity 85.7%; Pred. No. 8.1;
Matches 6; Conservative 1; Mismatches
                  C; Superfamily: silkworm pol protein
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57.1%;
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A,Genetic code: 8GC5
A,Introns: 280/3; 538/2; 1248/2
C,Superfamily: G surface protein
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Best Local Similarity 5/...
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2149 CIPITNC 2155
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550 CIPMTAC 556
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R.Tomb, J.F.; White, O.; Kerlavage, A.R.; Clayton, R.A.; Sutton, G.G.; Fleischmann, R.D. Peterson, S.; Loftus, B.; Richardson, D.; Dodson, R.; Khalak, H.G.; Glodek, A.; McKenne Son, J.D.; Kelley, J.M.; Cotton, M.D.; Weidman, J.M.; Fujii, C.; Bowman, C.; Watthey, L. Nature 388, 539-547, 1997.

A.Authors: Wallin, E.; Hayes, W.S.; Borodovsky, M.; Karpk, P.D.; Smith, H.O.; Fraser, C. A; Title: The complete genome sequence of the gastric pathogen Helicobacter pylori.

A.Reference number: A64520; MUID:97394467; PMID:9252185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A)Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-207 <TOM>
A;Cross-references: GB:AE000615; GB:AE000511; NID:g2314230; PIDN:AAD08133.1; PID:g23142:
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C.Species: Helicobacter pylori
A.Varietr in J99
C.Species: Helicobacter pylori
A.Varietr in J99
C.Species: D.S. in J99
C.Species: D.S. in J99
C.Species: D.S. in J993
C.Species: D.S. in J993
C.S. in J99
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A;Experimental source: strain J99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C;Species: Helicobacter pylori
C;Date: 09-Aug-1997 #sequence_revision 09-Aug-1997 #text_change 08-Oct-1999
C;Accession: A64655
                                                                                                                                                                                                      A;Residues: 1-191 <JEN>
A;Cross-references: EMBL:X73434; NID:g313719; PIDN:CAA51829.1; PID:g313720
C;Genetics:
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                       A; Reference number: I46412; MUID:94358466; PMID:7521375
                                                                  A;Accession: 146412
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 33;
Pred. No.
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C,Superfamily: ultra-high-sulfur keratin
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71.4%;
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Best Local Similarity
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Best Local Similarity
Matches 5; Conserv
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A;Molecule type: DNA
A;Residues: 1-207 <ARN>
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                                                                                                                                                                                                                                                                                                                                          CySpecies: Sus scrofa domestica (domestic pig)
CySpecies: Sus scrofa domestica (domestic pig)
CyDate: 02-Sep-2000 #sequence_revision 02-Sep-2000 #text_change 02-Sep-2000
CyAccession: T34022
R/Hardy, D.M.; Garbers, D.L.
J. Biol. Chem. 270, 26025-26028, 1995
A;Title: A sperm membrane protein that binds in a species-specific manner to the egg ext
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C;Date: 16-Aug-1996 #sequence_revision 16-Aug-1996 #text_change 24-Sep-1999
C;Accession: 146412; S34215
R;Jenkins, B.J.; Powell, B.C.
J:Invest. Dermatol. 103, 310-317, 1994
A;Title: Differential expression of genes encoding a cysteine-rich keratin family in the
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CiSpecies: Arabidopsis thaliana (mouse-ear cress)
CiSpecies: Arabidopsis thaliana (mouse-ear cress)
CiSpecies: 19-Mar-1997 #sequence_revision 25-Apr-1997 #text_change 24-Sep-1999
CiAccession: S66316, S5225.
Exituemmler, F.; Kirchner, M.; Teuber, R.; Dittrich, P.
Plant Mol. Biol. 29, 551-565, 1995
Aritle: Differential accumulation of the transcripts of 22 novel protein kinase genes A; Reference number: S6314; MUD:96123233; PMID:8534852
A; Accession: S66314
A; Molecule type: DNA
A; Residues: 1-55 cTHU>
A; Residues: 1-59 cTHU>
A; Residues: 1-59 cTHU>
A; Residues: 1-59 cTHU>
A; Residu
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A,Molecule type: mRNA
A)Residues: 1-2476 <HAR>
A)Cross-references: EMBL:U40024; NID:g1066465; PID:g1066466; PIDN:AAC48486.1
A)Experimental source: strain Meishan; testis
C)Genetics:
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keratin KAP5.4 - sheep
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A;Residues: 1-223 <WO2>
A;Cross-references: GB M37760; NID:g200963; PIDN:AAA40107.1; PID:g200964
A;Cross-references: GB M37760; NID:g200963; PIDN:AAA40107.1; PID:g200964
A;Cross-references: GB M375-21380
B;Wood, L.; Mills, M.; Hatzenbuhler, N.; Vogeli, G
B;Wood, L.; Mills, M.; Hatzenbuhler, N.; Vogeli, G
B;Wood, L.; Mills, M.; Hatzenbuhler, N.; Vogeli, G
A;Title: Serine-rich ultra high sulfur protein gene expression in murine hair and skin c
A;Reference number: A38346; MUD:91065960; PMID:2250030
A;Accession: B38346
A;Molecule type: DNA
A;Residues: 1-21, 'GGCGGGGGGGGCGCCCKPVCC', 22-40, 'GSS', 44-45, 'G', 47-48, 'S', 50, 'GSS',
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C;Species: Mus musculus (house mouse)
C;Date: 28-Uun-1991 #sequence_revision 28-Uun-1991 #text_change 24-Sep-1999
C;Accession: A38346
E;Wood, L.; Mills, M.; Hatzenbuhler, N.; Vogeli, G.
J Biol. Chem. 265, 21375-21380, 1990
A;Title: Serine-rich ultra high sulfur protein gene expression in murine hair and skin A;Reference number: A38346; MUID:91065960; PMID:2250030
                                                                                                                                                                                          C;Species: Musuculus (house mouse)
C;Species: Musuculus (house mouse)
C;Date: 31-Mar-1992 #text_change 24-Sep-1999
C;Accession: A38660; B38346
B;Mood, L.; Mills, M.; Hatzenbuhler, N.; Vogeli, G.
J; Biol. Chem. 266, 4024, 1991
A;Title: Serine-rich ultra high sulfur protein gene expression in murine hair and skin A;Reference number: A38660; MUID:91154184; PMID:1840598
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C.Species: saimiriine herpesvirus 1
A.Note: host Saimiri sciureus (common squirrel monkey)
C.Date: 31-Dec_1992 #sequence_revision 31-Dec-1992 #text_change 16-Jul-1999
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A;Cross-references: GB:M37759; NID:g200961; PIDN:AAA40106.1; PID:g200962
C;Superfamily: ultra-high-sulfur keratin
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A;Status: preliminary
A;Molecule type: DNA
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C;Superfamily: varicella-zoster virus gene 35 protein
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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OM protein - protein search, using sw model

5, 2004, 09:38:39; Search time 3.18182 Seconds (without alignments) 114.554 Million cell updates/sec September Run on:

US-09-761-636A-11 42 1 CVPLTSC 7 Title: Perfect score: Sequence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

141681 segs, 52070155 residues Searched:

141681 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt_42:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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90.5%; Score 38; DB 1; Length 383;
Best Local Similarity 85.7%; Pred. No. 2.2;
Matches 6; Conservative 1; Mismatches 0; Indels

P15692 homo sapien Q46809 escherichia P27512 mus muscullu P37190 escherichia 000220 homo sapien P41951 caenorhabdi P17053 paramecium P13817 paramecium Q97493 homo sapien Q13653 homo sapien P08997 dictyosteli P48304 homo sapien	S 44	te) date) Ype I retrotransposable sse (EC 2.7.7.49);	Endopterygota; Hymenoptera; Apocrita; Chalcidoidea; lae; Nasonia. 197425; ROM N.A. 196484; PubMed=8383793; Fickbush D.G., Xiong Y., Jakubczak J.L., Eickbush T.H.; relationship of retrofransposable elements	between divergent insect species."; Biol. Evol. 10:163-185(1993). CATALYTIC ACTIVITY: N deoxynucleoside triphosphate = N diphosphate	produced through a stics and the EMB sere are no restrict as its content is 1. Usage by and thtp://www.isb-sil	Transposable element;	REVERSE TRANSCRIPTASE. NUCLEIC ACID-BINDING ENDONUCLEASE. DE296B380925251B CRC64;
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232 286 289 346 468 1576 2704 2715 2715 2715 166	STANDARD;	001271, 01-JUN-1994 (Rel. 29, Created) 01-JUN-1994 (Rel. 29, Last sequence update) 16-CCT-2001 (Rel. 40, Last annotation update) Retrovirus-related POL polyprotein from type element R1 [Contains: Reverse transcriptase Endonuclease] (Fragment). Nasonia vitripennis (Parasitic wasp).	Neoptera; Endopterygota; Hymenoptera; Pteromalidae; Nasonia. NCBL TaxID=1425; (1) SEQUENCE FROM N.A. MEDLINE=93196484; PubMed=8383793; Burke W.D., Bickbush D.G., Xiong Y., "Sequence relationship of retrotransy."	and between divergent insect spec Mol. Biol. Evol. 10:163-185(1993) -!- CATALYTIC ACTIVITY: N deoxynu. + { DNA}(N).	Ting in it	Ø 54 · Ď Ed −	228 383 43411 MW;
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%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%	RESULT 1 PO13 NASVI ID PO13 NASVI	003271; 01-JUN-1994 (F 01-JUN-1994 (F 16-DCT-2001 (R Retrovirus-rel element R1 [C Endonuclease] Nasonia vitrip Eukarvota: Metri	Neoptera; Endopter Pteromalidae; Nas NCBI TaxID=7425; [1] SEQUENCE FROM N.A MEDLINE=93196484; Burke W.D., Eickbl "Sequence relation"	and bet Mol. Bi	This SWISS-PR between the the European use by non- modified and entities requ or send an em	EMBL; L00942; AAA303: PIR; D44490; D44490. InterPro; IPR000477; Pfam; PF00078; rvt; I Transferase; RNA-dire Hydrolase; Nuclease; NON TER	DOMAIN DOMAIN SEQUENCE
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                                                                                                                                                                                                                                                                                                                                        PEQUENCE OF 21-36.

TISSUE=Intestinal epithelium;

X MEDLINE=98180665; PubMed=9512496;

X Matri 1.A., Forstner G.G., Forstner J.F.;

X Matri 1.A., Forstner G.G., Forstner Tich N-terminal and C-terminal ends of "Susceptibility of the cysteine-rich N-terminal and C-terminal ends of "Susceptibility of the cysteine-rich N-terminal and C-terminal ends of "cat intestinal mucin Muc 2 to proteolytic cleavage.";

Electron J. 331:323-330(1998)

E. PUNCTION: Coats the epithelia of the intestines, airways, and other mucus membrane-containing organs. Thought to provide a protective, lubricating barrier against particles and infectious agents at mucosal surfaces.

C. SUBUNIT: Multimeric.

C. SUBLINIT: Multimeric.

C. SUBLINITY: Contains 1 VWFC domain.

C. SIMILARITY: Contains 3 VWFD domains.
                                                                                 Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                          Kim Y.S., Basbaum C.B.;
"Molecular cloning of the amino-terminal region of a rat MUC 2 mucin
gene homologue. Evidence for expression in both intestine and
                                                                                                                                                                                            MEDLINE-94299489; PubMed-8027037;
Ohmori H., Dohrman A.F., Gallup M., Tsuda T., Kai H., Gum J.R. Jr.,
Kim Y.S., Basbaum C.B.;
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Mucin 2 precursor (Intestinal mucin 2) (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPROXIMATE REPEATS.
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MUCIN 2.
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VWFC.
VWFD 2.
VWFD 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PROSITE; PS01208; VWFC_1; FALSE_NEG.
PROSITE; PS50184; VWFC_2; FALSE_NEG.
                                                                                                                                                                                                                                                                                                          Biol. Chem. 269:17833-17840(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; U07615; AAA21655.2;
PIR; A54895; A54895
InterPro; IPR00219; TIL Cysrich.
InterPro; IPR00219; TIL Cysrich.
InterPro; IPR001846; VWF_C.
InterPro; IPR011846; VWF_D.
Pfam; PF01826; TIL; 1.
Pfam; PF01826; TIL; 1.
SMART; SM00214; VWC; 3.
SMART; SM00214; VWC; 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Signal, Repeat; Glycoprotein.
                                                                         Rattus norvegicus (Rat).
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                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                       TISSUE=Intestine;
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                                                                                                                        NCBI_TaxID=16116;
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                                                                                                                                                                                                                                                                                                                                                                                                          -i- SUBCELLULAR LOCATION: Nuclear and associated with desmosomes (By
                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Bovinae; Bos.
                                                                                                                                                                                                                                                   MEDLINE-95196971; PubMed-7890138;
Heid H.W., Schmidt A., Zimbelmann R., Schaefer S.,
Winter-Simanowski S., Stumpp S., Keith M., Figge U., Schnolzer M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cell adhesion; Cytoskeleton; Structural protein; Nuclear protein;
                                                                                                                                                                                                                                                                                                                 "Cell type-specific desmosomal plaque proteins of the plakoglobin family: plakophilin 1 (band 6 protein)."; Differentiation 58:113-131 (1994).
--- FUNCTION: SEEMS TO PLAY A ROLE IN JUNCTIONAL PLAQUES (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ;
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GO; GO:00030563; C:desmosome; ISS.
GO; GO:0003215; F:intermediate filament binding; ISS.
GO; GO:0007155; F:erl adhesion; ISS.
GO; GO:0007155; P:esll adhesion; ISS.
GO; GO:0007155; P:signal transduction; ISS.
InterPro; IFR008938; ARM.
RIMERPRO; IFR00825; Armadillo.
PFam; PF00514; Armadillo.seg; 4.
SMART; SM00185; ARM; 5.
RPOSITE; PS50176; ARM; F.
RPOSITE; PS50176; ARM; F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 35; DB 1; Length 727;
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                                                                                                                                                                                                                                                                                                                                                                                                                                      similarity).
-!- SIMILARITY: Belongs to the beta-catenin family.
-!- SIMILARITY: Contains 8 ARM repeats.
                                             28-FEB-2003 (Rel. 41, Last sequence update) 28-FEB-2003 (Rel. 41, Last annotation update) Plakophilin 1 (Band-6-protein) (B6P).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT; 1513 AA.
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; Mismatches
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ARM 2.
ARM 3.
ARM 4.
ARM 5.
ARM 6.
ARM 6.
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28-FBB-2003 (Rel. 41, Created)
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                                   (Rel. 41, Created)
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727 AA;
                                                                                                                          Bos taurus (Bovine).
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Best Local Similarity
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SEQUENCE FROM N.A.
                                                                                                                                                                                                    NCBI_TaxID=9913;
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                  Q28161;
28-FEB-2003
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MUC2_RAT ID _MUC2_RAT

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                                                                                                                                                                                                                                    PROSITE; PS00022; EGF 1; 1.
PROSITE; PS00186; EGF 2; 4.
PROSITE; PS0026; EGF 3; 1.
PROSITE; PS00740; MAM 1; 1.
PROSITE; PS50066; MAM 2; 2.
Signal; Glycoprotein; Transmembrane; EGF-like domain; Cell adhesion; Repeat.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         V (IN REF. 1; AA SEQUENCE)
Y (IN REF. 1; AA SEQUENCE)
Y (IN REF. 1; AA SEQUENCE)
Y (IN REF. 1; AA SEQUENCE)
A13B690375A6548C CRC64;
                                                                                                                                                                                                                                                                                                                                                                MAM 2.
53 X HEPTAPEPTIDE REPEATS
(MUCIN-LIKE DOMAIN).
VWFD 1 (PARTIAL).
                                                                                                                                                                                                                                                                                                                 ZONADHESIN.
EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                               CYTOPLASMIC (POTENTIAL)
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VWED 5.
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EGF-LIKE.
BY SIMILARITY.
BY SIMILARITY.
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InterPro; IPR003328; TILa_Cysrich.
InterPro; IPR001007; VWF_C.
InterPro; IPR001846; VWF_D.
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MAM_domain.
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                                                                      EMBL; U40024; AAC48486.1; -.
PIR; T34022; T34022.
HSSP; P56682; 1CCV.
                                                                                                                                                       Pfam; PF00008; BGF; 1
Pfam; PF00629; MAM; 2.
Pfam; PF00629; TLL; 5.
Pfam; PF00245; TLL; 5.
Pfam; PF00094; vwd; 4.
SMART; SM00137; MAM; 1.
SMART; SM00214; vWC; 2.
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InterPro; IPR000998;
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                                                                                                                                                                                                                                                                                                                                                                         SUBURIT: Probably forms covalent oligomers.
SUBCELLULAR LOCATION: Type I membrane protein, exclusively on the apical region of the sperm head (By similarity).
TISSUB SPECIFICITY: In testis, primarily in haploid spermatids.
Not in lung, liver, heart, spleen, brain, kidney, epididymis.
DOMAIN: The MAM domains probably mediate sperm adhesion to the
                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DOMAIN: During sperm migration through the reproductive tracts, the mucin-like domain might inhibit inappropriate trapping of Spermatozoa or promoting adhesion to the oviductal isthmus. DOMAIN: The VWPD domains 2 and 3 may mediate covalent oligomerization (By similarity to human intestinal mucin MUC2). PTM: THE MAM DOMAINS AND THE MUCIN-LIKE DOMAINS ARE MISSING PROCESSING MIGHT OCCUR DURING SPERM MATURATION AND/OR
                                                                                                                                                                                                                                                                                                                                       Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
                     (POTENTIAL).
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(POTENTIAL).
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                                                                                                                                                                           1; Indels
                                                                                                                                    166036 MW; 26109DCA1BE7D008 CRC64;
                                                                  (GLCNAC. . .)
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                                                                                                                                                      Score 34; DB :
Pred. No. 56;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -!- SIMILARITY: Contains 2 MAM domains.
-!- SIMILARITY: Contains 5 VWFD domains.
-!- SIMILARITY: Contains 1 EGF-like domain.
           N-LINKED
                                                                                                                                                             71.48;
                                                                                                                                                      81.0%;
                                                                                                                                                                        5; Conservative
                    420
667
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1513 AA;
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CVPLSKC 715
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                                                                                                                                                               Best Local Similarity
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01-APR-1993
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01-APR-1993
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                                                                                                                RESULT 6
UL24 HSVSA
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                                                                               셤
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                       0
                                                                                                                                                                                                                                                                                                                                 "Keratin associated proteins (KAPs): Characterisation of a second high
                                                                                                                                                    15-WAR-2004 (Rel. 43, Created)
15-WAR-2004 (Rel. 43, Last sequence update)
15-WAR-2004 (Rel. 43, Last annotation update)
16-WAR-2004 (Reratin associated protein 10.10)
17-WAR-2004 (Representated protein 10.10)
                                                                                                                                                                                                                                                                                                                                           sulfur KAP gene domain on human chromosome 21.";
J. Invest. Dermatol. 0.0-0(2003)
-: FUNCTION: In the hair cottex, hair keratin intermediate filaments are embedded in an interfilamentious matrix, consisting of hair keratin-associated protein (KRTAP), which are essential for the formation of a rigid and resistant hair shaft through their extensive disulfide bond cross-linking with abundant cysteine extensive of hair keratins. The matrix proteins include the high-sulfur and high-glycine-tyrosine keratins.
-: SUBUNIT: Interacts with hair keratins.
-: TISSUE SPECIFICITY: Expressed exclusively in a narrow region of the middle portion of hair fiber cuticle.
-: SIMILARITY: Belongs to the KRTAP type 10 family.
                        Gaps
                                                                                                                                                                                                                                   Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; AL773602; -; NOT ANNOTATED CDS.

Genew; HGNC:22972; KRTAP10-10.

Keratin; Repeat; Multigene family.

DOMAIN 26 224 [SPTQA]-[SCAV].
                        ·.
                                                                                                                                                                                                                                                                                                  TISSUE=Scalp;
Rogers M.A., Langbein L., Winter H., Beckmann I., Praetzel S.
Schweizer J.;
Score 34; DB 1; Length 2476; Pred. No. 92;
                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A128CDBB45B74962 CRC64;
                                                                                                                                251 AA.
                         Mismatches
                                                                                                                                PRT;
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  81.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; AJ566387; CAD97467.1;
 Query Match
Best Local Similarity 71.4
Matches 5; Conservative
                                                                                                                                STANDARD;
                                                                        1505 CVPLSQC 1511
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 26
31
52
53
84
94
99
104
1168
1168
1168
202
222
221
24,
                                                                                                                                                                                                                              Homo sapiens (Human)
                                                 1 CVPLTSC 7
                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                 NCBI_TaxID=9606;
                                                                                                                                  K10A_HUMAN
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REPEAT
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                                                                    Gaps
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MEDLINE-9233688; PubMed=1321287;
Albrecht J.-C., Nicholas J., Biller D., Cameron K.R., Biesinger B.,
Newman C., Wittmann S., Craxton M.A., Coleman H., Fleckenstein B.,
Honess R.W.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Primary structure of the herpesvirus saimiri genome.";
J. Virol. 66:5047-5058(1992).
-!- SIMILARITY: BELONGS TO FAMILY THAT GROUPS TOGETHER HSV-1 UL24,
EHV-1 37, EBV BXRF1, HCMV UL76, ILTV ORF3, AND VZV 35.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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TISSUE=Placenta;
Isogai T., Ota T., Hayashi K., Sugiyama T., Otsuki T., Suzuki Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .,
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18;
                  78.6%; Score 33; DB 1; Length 251; 71.4%; Pred. No. 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1; Indels
                                                                       1; Indels
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SEQUENCE 303 Aa; 34942 MW; DF6D59F7A1C83A0B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Herpesvirus saimiri (strain 11).
Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
Gammaherpesvirinae; Rhadinovirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FEX3 HUMAN STANDARD; PRT; 471 AA. Q9UK99; QNUXZ; 16-0CT-2001 (Rel. 40, Created) 16-CCT-2001 (Rel. 40, Last sequence update) 10-0CT-2003 (Rel. 42, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                   (Rel. 25, Created)
(Rel. 25, Last sequence update)
(Rel. 25, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Mismatches
                                                                          Mismatches
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Pred. No.
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85.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; X64346; CAA45644.1; -.
Query Match
Best Local Similarity 71.4°,
5, Conservative
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Best Local Similarity 85.7
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                           STANDARD;
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Eukaryota; Metazoa;
                                                                                                                                                                              203 CVPVPSC 209
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                                                                                                                            1 CVPLTSC 7
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                                                                                                                                                                                                                                                                                                                                                                                                                                        Gene 20 protein.
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-!- FUNCTION: Binds in a species-specific manner to the zona pellucida of the egg. May be involved in gamete recognition and/or signaling (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -!- SUBUNIT: Probably forms covalent oligomers (By similarity).
-!- SUBCELUIAR LOCATION: Type I membrane protein, exclusively on the apical region of the sperm head (By similarity).
-!- DOMAIN: The MAM domains probably mediate sperm adhesion to the zona pellucida.
-!- DOMAIN: During sperm migration through the reproductive tracts,
                                      -!- SUBCELLUTAR LOCATION: Integral membrane protein (Probable).
-!- SIMILARITY: Belongs to the ZIP transporter (TC 2.A.5) family.
KE4/Catsup subfamily.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryotă, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Lagomorpha, Leporidae, Oryctolagus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         N-LINKED (GLCNAC. .) (POTENTIAL)
N-LINKED (GLCNAC. .) (POTENTIAL)
N-LINKED (GLCNAC. .) (POTENTIAL)
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                                                                                                                                                                                                                                                                                                                                                                          Transport; Transmembrane; Glycoprotein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Amilarity 71.4%; Pred. No. 30; Somilarity 71.4%; Pred. No. 30; S. Conservative 1; Mismatches 1; Indole
                  Submitted (OCT-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -LINKED (GLCNAC. . 17D7E854F4E1DAAF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  16-0CT-2001 (Rel. 40, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
10-0CT-2003 (Rel. 42, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HIS-RICH
                                                                                                                                                                                                                                                                                                         WormPep, H13N06.5; CE18815.
InterPro, IPR003689; Zn_transpt_Zip.
Pfam, PF02535; Zip; 1.
Hypothetical protein; Transport; Tran
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=21573741; PubMed=11717130;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Oryctolagus cuniculus (Rabbit).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         55500 MW;
                                                                                                                                                                                                                                                                          EMBL; Z99942; CAB17070.1; -. PIR; T23089; T23089.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
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515 AA;
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386
429
463
92
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ZAN_RABIT
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Nishikawa T., Nagai K., Sugano S., Aotsuka S., Yoshikawa Y., Matsunawa H., Ishii S., Kawai Y., Saito K., Yamamoto J., Wakamuts Y., Magahari K., Masuho Y., Sasaki N.; "NEDO human cDNA sequencing project."; "NEDO human cDNA sequencing project."; Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                            Curr. Biol. 9:1180-1182(1999).
-!-FUNCTION: Probably recognizes and binds to some phosphorylated proteins and promotes their ubiquitination and degradation.
-!- SUBUNIT: Part of a SCF (SKP1-cullin-F-box) protein ligase complex (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota, Metazoa, Nematoda, Chromadorea, Rhabditida, Rhabditoidea,
Rhabditidae, Peloderinae, Caenorhabditis.
NCBI_TaxID=6239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Genew; HGNC:1358, PRX03.

Genew; HGNC:1358, PRX03.

GO: 0004840; F: Pubiquitin conjugating enzyme activity; TAS.

GO: 00:004842; F: Pubiquitin.protein ligase activity; TAS.

GO: 00:006508; P: proteolysis and peptidolysis; TAS.

InterPro: IPR001474; DUF55.

InterPro: IPR001810; F-box.

Pfam; PF04379; DUF525, 1.

Pfam; PF04479; DUF525, 1.

PRWNT; SM00256; PSOX; 1.

PROSITE; PS50181; FBOX; 1.
                                                                                                                                                               Elledge S.J., Harper J.W.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              F-BOX.
ASP/GLU-RICH (HIGHLY ACIDIC).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 33; DB 1; Length 471; Pred. No. 28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            T -> A (IN REF. 2).
EM -> VS (IN REF. 2).
F7AA88193E14E67E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              15-WAR-2001 (Rel. 40, Last sequence update)
15-WAR-2004 (Rel. 43, Last annotation update)
Hypothetical Ke4-like protein H13N06.5 in chromosome X.
H13N06.5.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1; Mismatches
                                                                                                                  SEQUENCE OF 6-415 FROM N.A.
MEDLINE=20003061; PubMed=10531037;
Winston J.T., Koepp D.M., Zhu C., Elledge
"A family of mammalian F-box proteins.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             POLY-ARG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; AK001943; BAA91991.1; -.
EMBL; AF176702; AAF03702.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                415 E
54590 MW;
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16-OCT-2001 (Rel. 40, Last seq
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à g KEAL_CAREL ID KEAL_CY DT 16-0CT-DT 16-0CT-DT 15-0CT-DT 15-0CT-CO Hypoth GN H13N06 GN CARPOTH OC ENEADY OC ENEADY OC NEADING N N III RP SEQUEN RP SEQUEN RA LEADA

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CRC64;

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                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     26 X HEPTAPEPTIDE REPEATS (APPROXIMATE)
   the mucin-like domain might inhibit inappropriate trapping of spermatozoa or promoting adhesion to the oviductal isthmus.

-!- DOMAIN: The VWFD domains 2 and 3 may mediate covalent oligomerization (By similarity to human intestinal mucin MUC2).
-!- SIMILARITY: Contains at least 2 MAM domains.
-!- SIMILARITY: Contains 5 VWFD domains.
-!- SIMILARITY: Contains 1 RGF-like domain.
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INTERPRO, PAROGONA2; EGF 2.
INTERPRO; IPRO006209; EGF 1ike.
INTERPRO; IPRO005919; MAM_Gomain.
INTERPRO; IPRO003919; TILA CYSTICH.
INTERPRO; IPRO01907; VWF C.
INTERPRO; IPRO01046; VWF D.
PÉAM; PPO0008; EGF; 1.
PÉAM; PPO0008; EGF; 1.
PÉAM; PPO0008; EGF; 1.
PÉAM; PRO00245; TILA; 5.
PÉAM; PRO0134; VWC; 2.
SWART; SMO0114; VWC; 2.
SWART; SMO0114; VWC; 2.
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PROSITE; PS01186; EGF 2; 4.
PROSITE; PS0026; EGF 3; 1.
PROSITE; PS00740; MAM 1; FALSE NEG.
PROSITE; PS50060; MAM 2; 2.
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Score 33; DB 1; Length 2282;

78.6%;

Query Match

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -:- SIMILARITY: Contains 2 F5/8 type C domains.
-:- SIMILARITY: Contains 2 VWFC domains.
-:- SIMILARITY: Contains 1 C-terminal cystine knot-like (CTCK) domain.
                                                                                                                                                                                                                                                                                                                                                                                                                     Kotani E., Yamakawa M., Iwamoto S.-I., Tashiro M., Mori H., Sumida M., Matsubara F., Taniai K., Kadono-Okuda K., Kato Y., Mori H.; "Cloning and expression of the gene of hemocytin, an insect humoral lectin which is homologous with the mammalian von Willebrand
                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia; Bombycoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE OF 2221-3133 FROM N.A.

Kotani E., Iwamoto S.I., Tashiro M., Mori H., Sumida M.,

Matsubara F., Yamakawa M.;

Submitted (JAN-1993) to the EMBL/GenBank/DDBJ databases.

-!- FUNCTION: Adhesive protein and relates to hemostasis or encapsulation of foreign substances for self-defense.

-!- DEVELOPMENTAL STAGE: Expressed in hemocytes during larVal-pupal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                proteolysis.
-!- SIMILARITY: TO MAMMALIAN VON WILLEBRAND FACTOR.
-!- SIMILARITY: THE N-TERMINAL DOMAIN SHOWS SOME SIMILARITY TO THAT
OF HUMAN MUCIN 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              metamorphosis.
-!-INDUCTION: Hemagglutination activity is increased by bacterial or viral infection and inhibited by D-mannose, N-acetyl-D-galactosamine and D-maltose.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -!- PTM: May be converted into the 260 kDa mature hemocytin by
                                                                                                                                                                   01-FEB-1996 (Rel. 33, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
Hencytin precursor (Humoral lectin)
Bombyx mori (Silk moth)
                                                                                                                                   PRT; 3133 AA
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                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
STRAIN=Fuyou X Tokai; TISSUE=Hemocyte;
MEDLINE=95178544; PubMed=7873598;
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InterPro; IPR000421; FA58 C.
InterPro; IPR008179; Gal End like.
InterPro; IPR002172; IDL Ecceptor A.
InterPro; IPR02219; TIL Cysrich.
InterPro; IPR010007; WWF.C.
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Pfam; PF00754; F5_F8_type_C; 2.
Pfam; PF01826; TIL; 6.
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NCBI_TaxID=7091;
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Pfam; PF00094; vwd; 3.
SWART; SM00231; FASBC; 2.
SWART; SM00231; FASBC; 2.
SWART; SM00216; VWD; 3.
PROSITE; PS01185; CTCK 2; 1.
PROSITE; PS01285; CTCK 2; 1.
PROSITE; PS01285; FASBC 1; 2.
PROSITE; PS01286; FASBC 1; 2.
PROSITE; PS01286; FASBC 2; 2.
PROSITE; PS01208; VWFC 1; FALSE NEG.
Lectin; Glycoprotein; Signal; Repeat; Cell adhesion.
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Score 33; DB 1; Length 3133; Pred. No. 1.9e+02;

78.6%; 71.4%;

Query Match Best Local Similarity

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Tand polymorphism.";

J. Clin. Invest. 88:1005-1013(1991).

- FUNCTION: Coate the epithelia of the intestines, airways, and other mucus membrane-containing organs. Thought to provide a protective, lubricating barrier against particles and infectious of agents at mucosal surfaces.

- SIBUNIT: Multimeric.

- SIBUNIT: Multimeric.

- SIBURIT: Multimeric.

- TISSUE SPECIFICITY: COLON, SMALL INTESTINE, COLONIC TUMORS, BRONCHUS, CERVIX AND GALL BLADDER.

- FROW ALL CYSTEINE RESIDUES ARE INVOLVED IN INTRACHAIN OR INTERCHAIN DISULFIDE BONDS (BY SIMILARITY).

- POLYMORPHISM: The number of repeats is highly polymorphic and varies among different alleles.

- SIMILARITY: Contains 1 TIL (Trypsin inhibitory-like) domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "The human MUC2 intestinal mucin has cysteine-rich subdomains located both upstream and downstream of its central repetitive region."; J. Biol. Chem. 267:21375-21383(1992).
         Gaps
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MEDLINE-94132002; PubMed=8300571;
Gum J.R. Jr., Hicks J.W., Toribara N.W., Siddiki B., Kim Y.S.;
"Molecular cloning of human intestinal mucin (MCC2) cDNA.
Identification of the amino terminus and overall sequence similarity to prepro-von Willebrand factor.",
J. Biol. Chem. 269:2440-2446(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=91358717; PubMed=1885763;
Toribara N.W., Gum J.R. Jr., Culhane P.J., Lagace R.E., Hicks J.W., Petersen G.M., Kim Y.S.;
"MUC-2 human small intestinal mucin gene structure. Repeated arrays
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TISSUE=Colon;
TISSUE=93016075; PubMed=1400449;
Gum J.R. Jr., Hicks J.W., Toribara N.W., Rothe E.-M., Lagace R.E.,
Kim Y.S.;
                                                                                                                                                                                                                                                                                                             Eukaryota; Medazoa; Chordata; Craniaca; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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       Indels
                                                                                                                                                                               002817; 014878;
01-UVN-1994 (Rel. 29, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
01-NOV-1997 (Rel. 35, Last sequence update)
Musin 2 precursor (Intestinal mucin 2)
MUCZ OR SMUC.
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SEQUENCE OF 1343-1895 AND 4176-4195 FROM N.A.
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   Mismatches
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EMBL; M74027; AAAS9875.1; -.
EMBL; M94131; AAAS9163.1; -.
 5; Conservative
                                                                                                                                                                     STANDARD;
                                                                       203 CVPATOC 209
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                                    1 CVPLTSC 7
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                                                                                                                              RESULT 11
MUC2_HUMAN
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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MEDLINE-96424990; PubMed-8827441;

A Pham T.M., Hayashi K., Takano R., Hara S.;

A Itoh M., Eguchi M., Matsubara F., Hara S.;

T "Expression of Bombyx family fungal protease inhibitor F from Bombyx or "Expression of Bombyx (T mori by baculovirus vector.";

U. Biochem. 119:1080-1085(1996).

A Itoh M., Takenaka T., Ashikari T., Eguchi M.;

C STRAIN-C124; TISSUE-Fat body;

C STRAIN-C124; TISSUE-Fat body;

C TICh M., Takenaka T., Ashikari T., Eguchi M.;

TICh M., Takenaka T., Bahikari T., Eguchi M.;

TICH M., Takenaka T., Bahikari T., Bauchi M.;
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01-NOV-1997 (Rel. 35, Last sequence update)
10-0CT-2003 (Rel. 42, Last annotation update)
Fungal procease inhibitor F precursor (FPI-F).
Bombyx mori (Silk moth).
Bukaryota, Metazoa, Arthropoda, Hexapoda, Insecta; Pterygota;
Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia; Bombycoidea;
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Pred. No. 3.1e+02;
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71.4%;
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Best Local Similarity 71.4
Matches 5, Conservative
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NCBI_TaxID=7091;
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APPROXIMATE REPEATS.
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Genew; HGNC:7512; MUC2.
MIM; 158370; -.
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                                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                                                                                                   RESULT 14
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Matches
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                DAN TETERS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          P24392; Q63733;

01-MAR-1992 (Rel. 21, Created)

01-MAR-1992 (Rel. 21, Last sequence update)

16-0CT-2001 (Rel. 40, Last annotation update)

Peroxisome assembly factor-1 (PAF-1) (Peroxin-2) (Peroxisomal membrane
                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=91166637; PubMed=1750930; Tsukamato T., Miura S., Fujiki Y.; "Restoration by a 35K membrane protein of peroxisome assembly in a peroxisome-deficient mammalian cell mutant."; Nature 350:77-81(1991).
                                                                                                                                                                                                                                                                                                            ..
0
                                                                                                                          FUNGAL PROTEASE INHIBITOR F.
                                                                                                                                                                                                                                                                    Score 32; DB 1; Length 77;
Pred. No. 7;
                                                                                                                                                                                                                                                                                                         1; Indels
                                                                                                                                                                                                                               8492 MW; B9CFC085DDA10354 CRC64;
                                                                                                                                             REACTIVE BOND
                                                                                                                                                                                                                                                                                                     Mismatches
                                                                                                        POTENTIAL.
                                        EMBL; X57988; CAA41054.1; -.
EMBL; D30616; BAA06306.1; -.
EMBL; D30617; BAA06307.1; -.
EMR; B53782; B53782.
InterPro; IPR006845; Pex2 Pex12.
InterPro; IPR001841; Znf ring.
Pfam; PF04757; Pex2 Pex12; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PXMP3 OR PEX2 OR PAF1 OR PMP35.
                  EMBL; S83181; AAB46908.1; -.
EMBL; D38075; BAA22409.1; -.
                                                                                                                                                                                                                                                                  76.2%;
57.1%;
                                                                                                                                                                                                                                                                                                     4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
                                                                                                          22
77
52
57
77
77
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN=Sprague-Dawley;
                                                                                                                                                                                                                                                                                                                                                          |||::|
CVPISQC 77
                                                                                                                                                                                                                                                                                                                                      1 CVPLTSC 7
                                                                                                                                                                                                                                                                                   Local Similarity
                                                                                                                     23
51
25
36
40
59
77 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=10116;
                                                                                                                                                                        DISULFID
                                                                                                                                     ACT SITE
DISULFID
                                                                                                                                                                                                                            SEQUENCE
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                                                                                                                                                                                                                                    Length 305;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Powell-Coffman J.A., Firtel R.A., "Characterization of a novel Dictyostelium discoideum prespore-specific gene, PspB, reveals conserved regulatory
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 1; Length 379; 35;
                                                                                                                                                                                                                                                                                0; Indels
                                                                                                                                   244 284 RING-TYPE.
125 125 R -> P.
305 AA; 34767 MW; 249058A5A5A8EB54 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Dictyostelium discoideum (Slime mold).
Eukaryota; Mycetozoa; Dictyosteliida; Dictyostelium.
NCBL_TaxID=44689;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Development 120:1601-1611(1994).
-!- SIMILARITY: Contains 3 prespore motif repeats.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRESPORE PROTEIN B. PRESPORE MOTIF 1. PRESPORE MOTIF 2. PRESPORE MOTIF 3.
                                                                                                                                                                                                                               76.2%; Score 32; DB 1; 83.3%; Pred. No. 28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-0CT-1996 (Rel. 34, Created)
01-0CT-1996 (Rel. 34, Last sequence update)
15-WAR-2004 (Rel. 43, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      379 A.A.
                                                                                                                                                                                                                                                                            1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2; Mismatches
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      SMART;
      SMO0184;
      RING;
      1.

      PROSITE;
      PS00518;
      ZF RING
      1;
      1.

      PROSITE;
      PS00689;
      ZF RING
      2;
      1.

      Transmembrane;
      Peroxisome;
      Zinc-finger.

      TRANSMEM
      140
      159
      POTENTIAL.

      TRANSMEM
      195
      213
      POTENTIAL.

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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=94326657; PubMed=8050366;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         42719 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    76.28;
57.18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; S72639; AAC60506.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DictyBase, DDB018506; pspB
InterPro; IPR003645; Foln.
SMART; SM00274; FOLN; 1.
Glycoprotein; Repeat; Sporul
                                                                                                                                                                                                                                                                         5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                224 CIPLTS 229
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289 3
319 3
                                                                                                                                                                                                                        Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                    1 CVPLTS 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PSPB DICDI
P54704;
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                                                                                                                                      ZN FING
VARIANT
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                "The cDNA RPEL and monoclonal antibody HWB-50 define gene products whe cDNA RPEL and monoclonal pigment epithelium.";

Exp. Eye Res. 55:657-662(1992).
-!- FUNCTION: Could be a melanogenic enzyme (By similarity).
-!- FUNCTION: Could be a melanogenic enzyme (By similarity).
-!- TISSUE SPECIFICITY: Retinal pigment epithelium.
-!- TISSUE SPECIFICITY: Retinal pigment epithelium.
-!- SIMILARITY: BELONGS TO THE PMEL-17/NMB FAMILY.
-!- SIMILARITY: Contains 1 PKD domain.
                                                                                                                                                                                                                            Bos taurus (Bovine).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Bovinae; Bos
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    X 13 AA APPROXIMATE TANDEM REPEATS
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N-LINKED (GLCNAC. . .) (POTENTIAL).
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0
                                                                                             01-NOV-1997 (Rel. 35, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Melanocyte protein Pmel 17 (Retinal pigment epithelial-specific
protein) (Fragment).
SILV OR PMELL 7 OR RPEI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    76.2%; Score 32; DB 1; Length 491; 83.3%; Pred. No. 46; 1; Mismatches 0; Indels
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                         491 AA.
                         PRT;
                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
TISSUE-Retina;
MEDLINE-93122163; PubMed=1478275;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           51669 MW;
                                                                             (Rel. 35, Created)
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Matches 5; Conservative
                            STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Kim R.Y., Wistow G.J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI TaxID=9913;
                                                                             01-NOV-1997
                               PM17 BOVIN
Q06154;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REPEAT
DOMAIN
CARBOHYD
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REPEAT
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PM17_BOVIN

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Search completed: September 5, 2004, 09:56:08 Job time : 4.18182 secs

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2 VPLTSC 7

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Q8tf36 homo sapien
Q8n8u9 homo sapien
                                                                                                                                                   September 5, 2004, 09:46:09; Search time 15.8384 Seconds (without alignments) 139.448 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1017041
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                         1017041 seqs, 315518202 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SUMMARIES
                                                                                               OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q8IRB8
P90649
Q9GMW9
Q833X0
O18464
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P90589
Q27183
Q8CG65
Q90993
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Gapop 10.0 , Gapext 0.5
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O97887
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QBCJ69
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sp_mammal:*
sp_mhc:*
sp_organelle:*
sp_phage:*
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_unclassified:*
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sp_bacteriap:*
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sp_bacteria:*
sp_fung::*
sp_human:*
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                seq length: 0
seq length: 2000000000
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sp_rodent:*
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Q7tn57 mus musculu Q81ya6 homo sapien Q9xsv8 bos taurus Q8spm4 bos taurus Q8m1k0 crocuta cro P79927 xenopus lae Q8tes1 homo sapien	~ ~ ~ ~	u O	U9Zm/8 helicobacte Q6220 mus musculu Q64507 mus musculu Q81ku4 sorghum bic Q7vgx3 helicobacte Q92585 sainiriine	040640 SAINIIINE Q91vi9 mus musculu Q91ie4 mus musculu Q96q28 homo sapien Q86z38 mus musculu
Q7TN57 Q81YA6 Q9XSV8 Q8SPM4 Q8M1K0 P79927 Q8TES1	Q8WWQ8 Q8IUG9 Q7Z5N9 Q9Y6R7 Q38989	Watras Q86BW2 Q285R3 Q28583 Q25713 Q25713	Q62220 Q64527 Q8LKU4 Q7VGX3 O92585	091VI9 091IE4 096028 08BZJ8
4 4 9 9 9 1 7 1 1 3 1 3 1 3 1 3 1 3 1 3 1 3 1 3 1	4 4 4 4 II C	111111111111111111111111111111111111111	175	11.4.11
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ALIGNMENTS

RP MEDLINE=20196006; PubMed=10731132,
RAMARM M.D., Celliker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
Adams M.D., Celliker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Mamatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Bruton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Man K.H., Doyle C., Baxter E.G., Champe M., Pfeiffer B.D.,
RA Abril J.F., Agbayani A., An H.J., Andrews-Ffannkoch C., Baldwin D.,
RA Beson K.W., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beson K.Y., Bencs P.V., Benan B.P., Bhandari D., Bolshakov S.,
RA Burks K.C., Eusam D.A., Buller H., Cadieu E., Center A., Chandra I.,
RA Geblos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
A Dodgon K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Pangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X., Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila. Created)
Last sequence update)
Last annotation update) 575 AA. PRT; 01-MAR-2003 (TrEMBLrel. 23, 01-MAR-2003 (TrEMBLrel. 23, 01-OCT-2003 (TrEMBLrel. 25, CG32260-PA. PRELIMINARY;

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RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacled J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reses M.G.,
RA Reinert K., Remington K., Saunders R.D., Scheeler F., Shen H.,
RA Spier E., Siden Kiamos I., Simpson M., Strong R., Smith T.,
RA Spier E., Spradling A.C., Tarner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
RA Yeh R.F., Zaveri J.S., Zhan M., Zhong W., Zhou Q., Zhong L.,
RA Aylliams S.M., Woodager, Worley K.C., Wu D., Yang S., Yao Q.R., Ya J.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers B.W., Rubin G.M., Venter J.C.;
R. Science 287:2185-2195(2000).
                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.

Celniker S.E., Adams M.D., Kronmiller B., Wan K.H., Holt R.A.,

Celniker S.E., Adams M.D., Amanatides P.G., Brandon R.C., Rogers Y.,

Banzon J., An H., Baldwin D., Banzon J., Beeson K.Y., Busam D.A.,

Carlson J.W., Center A., Champe M., Davenport L.B., Dietz S.M.,

Carlson J.W., Center A., Champe M., Davenport L.B., Dietz S.M.,

Carlson K., Dorsett V., Doup L.E., Doyle C., Dresnek D., Farfan D.,

Rerriera S., Frise E., Galle R.F., Garg N.S., George R.A.,

Gonzalez M., Houck J., Hoskins R.A., Hoetin D., Howland T.J.,

Libegwam C., Jalali M., Kruse D., Li P., Mattei B., Moshrefi A.,

Libegwam C., Jalali M., Murphy B., Nelson C., Nelson K.A., Nunco J.,

Ronnachar T.C., Moy M., Murphy B., Nelson C., Nelson K.A., Nunco J.,

Ronnachar S., Pittman G.S., Puri V., Richards S., Scheeler F.,

Brapheron M., Strong R., Svirska R., Tector C., Tyler D.,

Stapleron M., Strong R., Svirska R., Tector C., Tyler D.,

Williams S.M., Zaveri J.S., Smith H.O., Venter J.C., Rubin G.M.;

Sequencing of Drosophila melanogaster genome ",

Submitted (WAR-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mistar S., Crosby M.A., Matthews B.B., Bayraktaroglu L., Campbell K., Mistar S., Crosby M.A., Kaminker J.S., Prochnik S.E., Smith C.D., Trapy J.L., Bergman C., Berman B., Carlson J.W., Celniker S.E., Clamp M., Drysdale R., Emmert D., Frise B., de Grey A., Harris N., Kronmiller B., Marshall B., Millburn G., Richter J., Russo S., Searle S.M., Gelbart W.M., Rubin G.M., Mungall C.J., Lewis S.E.; Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Adams M.D., Celniker S.E., Gibbs R.A., Rubin G.M., Venter C.J., submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
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FlyBase; FBG00052560; CG322560,
GG: GG: 0004265; F: CHymotrypsin activity; IEA.
GG: GG: 0004295; F: Crypsin activity; IEA.
GG: GG: 0006508; P: proteolysis and peptidolysis; IEA.
InterPro; IPR006604; CLIP.
InterPro; IPR001254; Peptidase_81.
InterPro; IPR001254; Peptidase_81.
InterPro; IPR001214; Peptidase_81.
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SMART; SMOO680; CLIP; 1.
SMART; SMOO020; Tryp. SPc; 1.
PROSITE; PSSO240; TRYPSIN. DOM; 1.
PROSITE; PSO0135; TRYPSIN. SER; 1.
SEOURNCE 575 AA; 62063 WW; 9D;
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SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bourgain-Guglielmetti F., Caron; "Molecular characterization of the D surface protein gene subfamily in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-MAR-2003 (TrEMBLrel. 25, Last annotation update)
Hypothetical protein.
Macaca fascicularis (Crab eating macaque) (Cynonigus monkey).
Malexypota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Primates; Catarrhini; Cercopithecidae;
Cercopithecinae; Macaca.
                                                                                                                                                                                                                                                                                                                                    Paramecium primaurelia.
Eukaryota, Alveolata; Ciliophora; Oligohymenophorea, Peniculida;
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BMBL; AB047606; BAB12130.1; -.
Hypothetical protein.
SRQUENCE 127, AA; 12961 MW; EE168525256992CO CRC64;
                                                                                                                                                                                                                                                        Last sequence update)
Last annotation update)
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85.7%; Pred. No. 2.8;
tive 1; Mismatches
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                                                                                                                                                                               PRT; 2543 AA.
                                                                                                                                                                                                                                     Created)
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03,
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01-MAY-1997 (TrEMBLrel.
01-JUN-2003 (TrEMBLrel.
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2158 CIPITSC 2164
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204 CLPLTSC 210
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1 CVPLTSC 7
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STRAIN=ATC27405;
Kawaguchi T., Ikeuchi Y., Tsutsumi N., Kan A., Sumitani J., Arai M.;
"Cloning, nuclectide sequence, and expression of the Clostridium
thermocallum cellodextrin phosphorylase gene and its application to
J. Ferment. Bioeng. 85:144-149(1998).
EMBL; AB006822; BAA22081.1; -.
PIR; T00045; T00045.
InterPro, IPR008928; Glyco trans 6hp.
SEQUENCE 980 AA; 111183 MW; BARCREE3F5370831 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae; Clostridium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Paramecium tetraurelia.
Eukaryota, Alveolata, Ciliophora, Oligohymenophorea, Peniculida,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             85.7%; Score 36; DB 2; Length 980; 57.1%; Pred. No. 42; 1.1ve 3; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Schwegman K., Klein H., Schmidt H.; Schwegman K., Klein H., Schwidt H.; Submitted (MAR-1996) to the EMBL/GenBank/DDBJ databases. EMBL; X96400, CA465264.1; -. PIR, T28675, T28675.

FIR, T28675, T28675.

FinterPro; IRR002895, Paramecium SA.

Fam; PF01508; Paramecium SA.

SMART; SM00659; PSA; 26.

SEQUENCE 2533 AA; 264142 MW; EAED7F21E408C371 CRC64;
                                         UNKNOWN PROTEIN.
; 5CCA0924118D8FC6 CRC64;
                                                                                                                                                                                                                                                                                                                                                               Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-MAY-1997 (TYEMBLrel. 03, Created)
01-MAY-1997 (TYEMBLrel. 03, Last sequence update)
01-UN-2003 (TYEMBLrel. 24, Last annotation update)
Alpha-51D immobilization antigen.
                                                                                            B5.7%; Score 36; DB 5; 71.4%; Pred. No. 17; Live 2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT; 2533 A.A.
                       POTENTIAL.
                                                                                                                                                                                                                                                                                                                                               Created)
                                                          35617 MW;
Hypothetical protein; Signal.
                                                                                                                                                                                                                                                                                                                                       01-JAN-1998 (TrEMBLrel. 05, 01-JAN-1998 (TrEMBLrel. 05, 01-OCT-2003 (TrEMBLrel. 25, Cellodextrin phosphorylase.
                                                                        Query Match
Best Local Similarity 71.4%,
For Similarity 71.4%,
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Best Local Similarity 57.1-
4; Conservative
                                                                                                                                                                                                                                                                                                      PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                     Clostridium thermocellum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
                     337
                                                                                                                                                                                              199 CVPISSC 205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           550 CIPMTAC 556
                         SIGNAL 1
CHAIN 19
SEQUENCE 337 AA;
                                                                                                                                                                        1 CVPLTSC 7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=1515;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 CVPLTSC
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P90589
 SHFX
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                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
STRAIN=VS83 / ATCC 700802;
MEDLINE=22550857; Pubmed=12663927;
Paulsen I.T., Baneriei L., Myers G.S.A., Nelson K.E., Seshadri R., Read T.D., Fouts D.E., Bisen J.A., Gill S.R., Heidelberg J.F., Tettelin H., Dodson R.J., Umayam L., Brinkac L., Beanan M., Daugherty S., DeBoy R.T., Durkin S., Kolonay J., Madupu R., Nelson Vamathevan J., Tran B., Upton J., Hansen T., Shetty J., Khouri H., Utterback T., Radune D., Ketchum K.A., Dougherty B.A., Fraser C.M.; "Role of mobile DNA in the evolution of vancomycin-resistant
                                                                                                                                                                                            Enterococcus faecalis (Streptococcus faecalis).
Bacteria; Firmicutes; Lactobacillales; Enterococcaceae; Enterococcus.
NCBI_TaxID=1351;
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"A novel gene containing multiple EGP-like motifs transiently expressed in the papillae of the ascidian tadpole larvae.";
EMBL, U82540; AAB67704.1; -.
InterPro; IPR005210; IEGF.
InterPro; IPR005210; IEGF.
Pfam; PP01826; TIL, 4.
SMART; SM00181; EGF; 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Match
Local Similarity 71.4%; Pred. No. 17;
Es 5; Conservative 2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              68456 MW; 4940914DE5174E0D CRC64;
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Stolidobranchia, Pyuridae, Herdmania.
                                                                              0833X0;
01-JUN-2003 (TrEMBLrel. 24, Created)
01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Glycosyl hydrolase, family 35.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   60; GO:0003941; C:beta-galactosidase complex; IEA.
GO; GO:0004565; F:beta-galactosidase activity; IEA.
GO; GO:0016787; F:hydrolase activity; IEA.
GO; GO:0005975; P:carbohydrate metabolism; IEA.
InterPro; IPR001944; Glyco_hydro_35.
PRINTS; PR00742; GLHYDRLASB35.
Hydrolase; Complete proteome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-JAN-1998 (TrEMBLrel. 05, Created)
01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Hypothetical protein precursor.
                                                                    594 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           337 AA
                                                                    PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Herdmania momus (Brown sea squirt).
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Enterococcus faecalis.";
Science 299:2071-2074(2003).
EMBL; AE016952; AAO81573.1; -.
                                                                PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
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485 CLPMTSC 491
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TIGR;

RESULT 4
20833X0
ID 20833X0
DT 01-01
DT 01-01
DT 01-01
DT 01-01
DE GIYCC
GN EFIS
ON EFIS
ON NCBL
RA PAUL
RA PAUL
RA PAUL
RA DAUG
RA TECT
RA DAUG
RA DA

018464;

RESULT 5
018464
AC 01844
AC 0184,
DT 01-0.
DT 01-0.
DE HYDO
GN HECK
OC SUKA
OC SUKA
OC STOR
OX NCBI
RR SEQU
RR SEQU
RR STEQU
RR DEV.
DR DEN INTE

018464

Matches

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Gaps

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HSSP, P00523; 1SRL.
GO; GO:0007242; P:intracellular signaling cascade; IEA.
Interpro; IPR000980; SH2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      E) PS01225; CTCK 2; 1.

E) PS01186; EGF 2; 2.

E) PS01025; FA58C 3; 1.

E) PS01209; LDLRA_1; 8.

E) PS01209; LDLRA_1; 8.

E) PS50092; TSP1; 25.

E) PS50184; WWPC_1; 1.

E) PS50184; WWPC_2; 2.
                                             INTERPRO 1 LEVOUGAZI, FASS C. INTERPRO 1 LEVOUGAZI, FASS C. INTERPRO 1 PRO01545; GIY DOTMODEB. INTERPRO 1 PRO02192; IDL FOCEPTO. INTERPRO 1 PRO002919; ILL CYSTICH. INTERPRO 1 PRO00884; TSP 1. INTERPRO 1 PRO00885; TSP 1. INTERPRO 1 PRO01007; VWF D. INTERPRO 1 PRO01007; VWF D. PEAM; PRO0795; FS FS LYPE C. INTERPRO 1 PRO01007; ILL FOREST C. ILL FEAM; PRO0095; ILL FOREST C. ILL FEAM; PRO0099; TSP C. ILL FOREST C. ILL FEAM; PRO0099; TSP C. ILL FOREST 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     PROSITE; PS00196; COPPER_BLUE; 1.
Cys_knot_C.
                                                                                                                                                                                                                                                                                                                    PRINTS; PRO0261; IDLAECEPTOR.
PRINTS; PRO1705; TSPIREPEAT.
SMART; SM00192; LDLa; 10.
SMART; SM00209; TSPI; 25.
SMART; SM00214; VWC; 4.
SMART; SM00215; VWC; 0ut; 9.
                 like.
                                 FA58
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                     interPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PROSITE;
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PROSITE;
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Q90993
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                                                               Gaps
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Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A GONCALDER, TISSUE-Brain,
A GONCALVER, Simon-Chazottes D., Creveaux I., Meiniel A.,
GUENET J.L., Meiniel R.; Simon-Chazottes D., Creveaux I., Meiniel A.,
GUENCA J.L., Meiniel R.; Simon-Chazottes D., Creveaux I., Meiniel A.,
Guenet J.L., Meiniel R.,
Characterization, spatio-temporal expression and chromosomal
T "Characterization, spatio-temporal expression and chromosomal
E senignment of mouse SCO-spondin.";
Submitted (JUN-2002) to the EMBL/GenBank/DDBJ databases.
E EMBL; AJ491877 CAD4554.1;
R GO; GO:0005507; C:0xtracellular; IEA.
R GO; GO:0005507; F:copper ion binding; IEA.
R GO; GO:0005179; F:hormone activity; IEA.
R GO; GO:0005179; F:hormone activity; IEA.
R GO; GO:0005189; P:electron transport; IEA.
R GO; GO:000118; P:electron transport; IEA.
InterPro; IPR000923; BlueCu_1.
                                                                                                                                                                                                                                                                                                                                                      Paramecium tetraurelia.
Bukaryota; Alveolata; Ciliophora; Oligohymenophorea; Peniculida;
Paramecium.
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0
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85.7%; Score 36; DB 5; Length 2533;

Best Local Similarity 57.1%; Pred. No. 96;

Matches 4; Conservative 3; Mismatches 0; Indels
                       DB 5; Length 2533;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN=51;
Schmidt H.J.;
Submitted (MAR-1995) to the EMBL/GenBank/DDBJ databases.
EMBL, X88135; CAA59447.1; -.
PIR, T28674; T28674; T28674.
InterPro. IPR002895; Paramecium SA.
Pfam; PR01508; Paramecium SA.
SMART; SM00639; PSA; 26.
SEQUENCE 2533 AA; 263996 MW; 261BD09806BC344D CRC64;
                                                               0; Indels
                                                                                                                                                                                                                                                       Q27183;
01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Alpha-51D-immobilization antigen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Last sequence update)
Last annotation update)
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                       Score 36; DB 5
Pred. No. 96;
3; Mismatches
                                                                                                                                                                                                                                       PRT; 2533 AA
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01-MAR-2003 (TrEMBLrel. 23, Cr
01-MAR-2003 (TrEMBLrel. 23, La
01-OCT-2003 (TrEMBLrel. 25, La
SCO-spondin.
                       h 85.7%;
Similarity 57.1%;
4; Conservative
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2149 CIPITNC 2155
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2149 CIPITNC 2155
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                             Query Match
Best Local Similarity
                                                                                                      1 CVPLTSC 7
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Q8CG65
                                                                   Matches
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Q27183
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TISSUB=Percoralis muscle;
MEDLINE=90318371; PubMed=2115117;
MEDLINE=90318371; PubMed=2115117;
Dorai T., Mang L.-H.;
An alternative non-tyrosine protein kinase product of the c-src gene in chicken skeletal muscle.";
Mol. Cell. Biol. 10:4068-4079(1990).
-- SIMILARITY: CONTAINS 1 SH3 DOWAIN.
EMBL, M57290; AAAAONTINS 1. --
PIR; A00630; TUCHS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gallus gallus (Chicken).
Gukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                               Gaps
                                                                                                                                                               ;
0
                                                                                          Length 4998;
                                                                                          Query Match

85.7%; Score 36; DB 11; Length 49

Best Local Similarity 71.4%; Pred. No. 1.7e+02;

Matches 5; Conservative 2; Mismatches 0; Indels
550184; VWFC_2; 2.
4998 AA; 535019 MW; DAZABABDA47DF225 CRC64;
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
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RX MEDLINE=21085660; PubMed=11217851;
RX MEDLINE=21085660; PubMed=11217851;
RA Arakawa T., Hara A., Fukunishi Y., Konno M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saato R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Yamanaka I.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Kuchl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Kuchl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Kuchl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Kuchl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Blake J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Lyons P., Marchionni L., Machima J., Mazzarelli J., Mombaerts P.,
RA Gustincich S., Hill D., Hofmann M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Wilttaker C., Wilming L.,
RA Hayashizaki Y.,
RY "Functional annotation of a full-length mouse cDNA collection.",
RY. Narinze Ang. KRE.
                                                                                                                                                                      MEDLINES 922846; Pubmed-9560467;
Nualart F., Hein S., Yulis C.R., Zarraga A.M., Araya A.,
Nualart F., Hein S., Yulis C.R., Zarraga A.M., Araya A.,
Rodriguez E.M.;
"Partial sequencing of Reissner's fiber glycoprotein I (RF-Gly I).";
Cell Tissue Res. 292:239-250(1998).
EMBL; AF0789303. AAD17695.1; -.
HSPP; P56682; ICCV.
GO; GO:0005576; C:extracellular; IEA.
GO; GO:0005579; F:hormone activity; IEA.
InterPro; IPR001546; Gly_hormoneB.
InterPro; IPR002919; TIL_Cysrich.
InterPro; IPR00284; TSPI.
                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea; Bovidae; Bovinae; Bos.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              389 AA; 40720 MW; 48571E1F16F9F1B6 CRC64;
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Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             83.3%; Score 35; DB 6;
71.4%; Pred. No. 31;
live 2; Mismatches (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        462 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                              Interpro; IPRO00884; TSPI.
Pfam; PF01826; TIL; 1.
Pfam; PF00190; tSpI.; 1.
SMART; SM00209; TSPI.; 1.
PROSITE; PS00261; GLYCO_HORMONE_BETA_1; 1.
PROSITE; PS50092; TSPI; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-JUN-2001 (TrEMBLrel. 17, Created) 01-JUN-2001 (TrEMBLrel. 17, Last seq 01-JUN-2003 (TrEMBLrel. 24, Last ann 3110056H04Rik protein.
                                                                                                                                                        TISSUE=Subcommissural organ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              311 CVPVSŠC 317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CV2 OR 3110056H04RIK.
Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity
les 5; Conserv
                                                                                                                                   FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 CVPLTSC 7
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SEQUENCE
                                                                                                                                   SEQUENCE
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Q9CXM8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN=GPIC;
MEDLINE=22569155;
PLOMMEDLINE=22569155;
Read T.D., Myers G.S.A., Brunham R.C., Nelson W.C., Paulsen I.T.,
Heidelberg J., Holtzapple E., Khouri H., Federova N.B., Carty H.A.,
Umayam L.A., Haft D.H., Peterson J., Beanan M.J., White O.,
Salzberg S.L., Hsia R.-C., McClarty G., Rank R.G., Bavoil P.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GPIC):
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Genome sequence of Chlamydophila caviae (Chlamydia psittaci GPIC):
examining the role of niche-specific genes in the evolution of the
Chlamydiaceae,";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bacteria; Chlamydiae; Chlamydiales; Chlamydiaceae; Chlamydophila.
NCBI_TaxID=83557;
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                                                                                                                                                                                                                                                                                                                                 Length 193;
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                                                                                                                                                                                                                                                                                                                                                                            1; Indels
                                                                                                                                                                                                                                                                               9D1BE54C33B02D98 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Autolic Access. 31:2134-2147(2003).

BMBL; AB016995; AAP05172.1; -.

TIGR; CCA00426; -.

Interpro; IPR002589; Alpp.

SMART; SM00506; Alpp. 1.

Hypothetical protein; Complete proteome.

SEQUENCE 379 AA; 40634 MW; 62879277DBADD55D CRC64;
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Last annotation update)
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01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-UJV-2003 (TrEMBLrel. 24, Last annotation update)
Reissner's fiber glycoprotein I (Fragment).
Bos taurus (Bovine).
                                                                                                                                                                                                                                                                                                                          83.3%; Score 35; DB 13; 71.4%; Pred. No. 17;
                                                                                                                                                                                                                                                                                                                                                                       1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   389 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Created)
                                                                                                                                                                                                                                                                          193 AA; 21180 MW;
           Pfan; PF00017; SH2; 1.
Pfan; PF00018; SH3; 1.
PRINTS; PR00401; SH3DOMAIN.
PRINTS; PR00465; SH3DOMAIN.
ProDom; PD000093; SH2; 1.
ProDom; P0000066; SH3; 1.
SWART; SW00252; SH2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-JUN-2003 (TrEMBLrel. 24, 01-JUN-2003 (TrEMBLrel. 24, 01-OCT-2003 (TrEMBLrel. 25,
  IPR001452; SH3.
                                                                                                                                                                                                     PROSITE; PS50001; SH2; 1.
PROSITE; PS50002; SH3; 1.
SH3 domain.
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                                                                                                                                                                                                                                                                                           Hypothetical protein.
CCA00426
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Chlamydophila caviae.
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                                                                                                                                                                                                                                                                                                                                                                                                                  1 CVPLTSC 7
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InterPro;
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097887 RESULT 12 097887 ID 09788 AC 09788 DT 01-MA DT 01-MA DT 01-JA DE Reissi OS Bos tr

Matches

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Length 389; Indels

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Best Local Similarity
Matches 4; Conserv
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                                                                      Q8N8U9;
                                                  Q8N8U9
            RESULT 15
QBN8U9
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Nagase T., Kikuno R., Ohara O.;
"Prediction of the coding sequences of unidentified human genes. XXII. The complete sequences of 50 new cDNA clones which code for large
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                Gaps
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Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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                                                                                                                                                                                                                                                                                      Query Match

83.3%; Score 35; DB 11; Length 462;
Best Local Similarity 71.4%; Pred. No. 36;
Matches 5; Conservative 2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NON TER 1 1
SEQÜENCE 565 AA; 62934 MW; 1F7A15206F2B9D45 CRC64;
                                                                                                                                                                                                                                                    462 AA; 51641 MW; 5B6AF92A52D7A4B6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              QRTF16;
01-UUN-2002 (TrEMBLrel. 21, Created)
01-UUN-2002 (TrEMBLrel. 21, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Hypothetical protein KIAA1965 (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       procedure. Sequences of the complete sequenc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            565 AA
EWBL, AKO14221; BAB29213.1; -. HSSP; POO214; IFTC.
MGD, MGI:1920480; CV2.
INCERPIC: IPRO0199; TIL_Cysrich.
InterPro; IPRO01007; VWF_C.
InterPro; IPRO01007; VWF_D.
Pfam; PFO0093; VWC; 2.
Pfam; PFO0093; VWC; 2.
SWART; SW00214; VWC; 2.
SWART; SW00216; VWD; 1.
PROSITE; PS012084; VWCC_2; 1.
SROGNER; PS012084; VWCC_2; 1.
SROGNER; PS012084; VWFC_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 57.1.
A; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                 113 CVPVSSC 119
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Ninomiya K., Wagatsuma M., Kanda K., Kondo H., Yokoi T., Kodaira H., Furuya T., Takahaahi M., Kikkawa E., Omura Y., Abe K., Kamihara K., Furuya T., Takahaahi M., Yamazaki M., Sugiyama T., Irie R., Otsuki T., Sato K., Wakamatsu A., Ishii S., Yamanoto J., Isono Y., Kawai-Hio Y., Saito K., Nishikawa T., Kimura K., Yamashita H., Marsuo K., Nakamura Y., Sekine M., Kikuchi H., Murakawa K., Kanehori K., Takahashi-Fujii A., Oshima A., Sugiyama A., Kawakami B., Suzuki Y., Sugano S., Nagahari K., Masuho Y., Nagai K., Isogai T., Nabo human cDNA sequenching project.";
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Binnerts M.E., Wen X., Cante-Barrett K., Bright J., Chen H.-T.,
Bunnerts M.E., Wen X., Cante-Barrett K., Bright J., Chen H.-T.,
Asundi V., Sattari P., Tang T., Boyle B., Funk W., Rupp F.;
Submitted (JUN-2003) to the EMBL/GenBank/DDBJ databases.
BEBL; AX956150; BAC04712.1;
BMBL; AX934650; AAP89012.1;
BMBL; AX934650; AAP89012.1;
BMC GO; GO:0005509; F:calcium ion binding; IEA.
BRITEPPO; IPR000294; VitK dep_GLA.
InterPro; IPR001946; VWF C.
BRITEPPO; IPR001946; VWF D.
BRITEPPO; IPR001946; VWF D.
BRITEPPO; IPR001946; VWF D.
BRITEPPO; BRO0194; VWF, G.
BRITEPPO; BRON194; VWF, G.
BRON194; VWF,
                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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SEQUENCE 685 AA; 75996 MW; A5048AADEBF04ABO CRC64;
                                                                                               01-0CT-2002 (TrEMBLrel. 22, Created)
01-0CT-2002 (TrEMBLrel. 22, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
Hypothetical protein FLJ38831 (Crossveinless-2)
Homo sapiens (Human)
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Similarity 57.1%; Pred. No. 50;
4; Conservative 3; Mismatches (
685 AA
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PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             336 CIPISSC 342
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216 ČIPISŠČ 222

OM protein - protein search, using sw model

5, 2004, 09:37:49 ; Search time 22.9798 Seconds (without alignments) 86.068 Million cell updates/sec September Run on:

US-09-761-636A-11

Title:

1 CVPLTSC 7 Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

1586107 seqs, 282547505 residues Searched:

1586107 Total number of hits satisfying chosen parameters:

seq length: 0 seq length: 200000000 Minimum DB Maximum DB

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

geneseqp2000s:*
geneseqp2001s:*
geneseqp2002s:*
geneseqp2003as:* A Geneseq 29Jan04:* geneseqp1980s:* geneseqp1990s:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

geneseqp2004s:*

SUMMARIES

		Description		- (obs Propionib		_	,	Τ.	'58 Propionib		64 Novel hum	Human	Te HILL	Morroll	TACAGE	n (1 Propic	 (1)	Human	63 Novel pro	62 Human gen	Human	19 Human qen	3 Human	THIMPS C	T Human	23 Novel	
		Descri		Aduog	Adubzob	ADMS908	Abg13170	ADDIEC	Aau6423	Abm60758	Abg3020;	Abg21064	Aam9656	Ahhaksk	Too Lite A	ACCEPTED TO STATE OF THE STATE	Admoto	Aau4901	Abm45531	Aam9993	Abg6508	Ade07963	Aae0706	Abg65086	Aae071	Aau9929	Aau9929	Ahii118	Ade079	
		. QI	AAU04530		ABM59081	ARG13170	ABBITOAN	MATTER 230	ST COLUMN	100 000 D	ABG3 UZ U3	ABG21064	AAM96565	ABB96569	AAU18859	AAM94953	AA1149012		AMMODOO	ADCC 0000		1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	AAEU / U62	æ,	٠,	AAU99293	AAU99292	ABU11857	ADE07923	
		DB	4	4							•	4.	4	4	4	4	4	, ,		•	, ,		•	n .					•	
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*	Query	Match	100.0	90.5	٥.	90.5	m	85.7	10	110		•	•	•	•	83.3	•			83.3		•	•	0 0			83.3		83.3	
		Score	42	38	38	38	3.7	36	36	36	9 6	9 6	010	3,5	32	35	35	35	35	35	20	3.5	, c	י ני) C) L	0 °	35	32	
	esult	No.	н	7	е	4	Ŋ	9	7	α	σ	, ,	7 -	11	7.5	13	14	15	16	17	18	19	20	2.5	20	1 (7 .	24	52	

		Cycoskere	Drogophi	N. gonorr	Human imm	Drogonhil	. ,-		Drawing alb	gluordora	Propionib	Propionih	Propionih	A1101010	311-1-000	ALLOIOCOC	Novel hum	Morrel him		Novel pro	Human uro		
000000	AG055001	AUC36321	ADD/08/8	App77249	Aam86679	Abb64274	AAP04225	Abde A ov	4000000	Serotupa de	ADM44718	Aau42623	Abm39142	Adh06446	OFF COMPL	Auto 0440	Abg08337	Ahazakak	200000		Abb98302	Aba72514	Abi10587
AA029572	ADC56921	ABB70878	0.0000	ADF / /24 9	AAM86679	ABB64274	AAE04225	ABG64494	AA1148199	ABM44719	OT/ FEIGH	AAU42623	ABM39142	ADB06446	ADRO644R	7500000	7550000	ABG23698	ADE09017		ABB98302	ABG72514	ABJ10587
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745	745	3680	o di	י ר ר	65	88	89	89	95	ď	1	177	127	134	146	256	1 1	351	351	1046	0 7 7 7	1653	2420
83.3	83.3	83.3	5		0.18	81.0	81.0	81.0	81.0	81.0		0.10	81.0	81.0	81.0	6		91.0	81.0	ς C	0.10	81.0	81.0
35	35	35	3.4	1 5	ο (34	34	34	34	34		# ·	3.4	34	34	34	, ,	7,	34	3.4	,	34	34
26	27	28	59		7 (31	32	33	34	35	3,6) t	3,	89	39	40	,	7	42	43	, ,	4	45

ALIGNMENTS

AAU04530 standard; peptide; 7 AA. VEGF based monocyclic peptide 8. (first entry) 26-SEP-2001 AAU04530;

Human; VEGF; vascular endothelial growth factor; angiogenesis; neovascularisation; lymphangiogenesis; psoriasis; tumour; diabetes induced neovascular sequelae; rheumatoid arthritis; diabetic retinopathy; chronic inflammation; cyclic.

Synthetic.

Location/Qualifiers
1. .7
/note= "This bond cyclises the peptide" 18-JAN-2001; 2001WO-US001533. Key Disulfide-bond WO200152875-A1. 26-JUL-2001.

(LUDW-) LUDWIG INST CANCER RES. 18-JAN-2000; 2000US-0176293P. 16-MAY-2000; 2000US-0204590P.

Stacker S, Hughes RA, Achen MG,

Cendron A;

WPI; 2001-442248/47.

Novel monomeric monocyclic peptide, used to interfere with angiogenesis, or lymphangiogenesis, is produced by cyclizing a peptide loop fragment from an exposed loop of a growth factor protein by oxidizing the cysteine residues.

Claim 49; Page 32; 102pp; English.

The sequence represents a monomeric monocyclic peptide of the invention, whose 3-dimensional structure is modelled on the expose loop of human VEGFD (vascular endothelial growth factor). The invention relates to a method of producing a monomeric monocyclic peptide by a measuring betabeta carbon separation distances on opposite antiparallel strands of a

Example 1; SEQ ID NO 23757; 1069pp; English.

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peptide loop fragment from an exposed loop of a growth factor protein and cyclising the peptide by oxidising the cysteine residues. The monocyclic peptides, dimeric bicyclic peptides (comprising 2 linked monocyclic peptides) and a cyclic peptide with at least one anino acid deleted prior to cyclisation are used to interfer with angiogenesis, consistent on a lymphangiogenesis in a mammal with a condition carried by angiogenesis, neovascularisation or lymphangiogenesis, neovascularisation or lymphangiogenesis. The condition is diabetic retinopathy, psoriasis, arthropathy, cerebrovascular accident, post-angioplasty restenosis, heat or cold cramma, substance-induced melignant or benign tumour, post-recovery carried angiogenic dysfunction, diabetes induced neovascular cyclic hormone-related angiogenic dysfunction, diabetes induced neovascular cyclic in a mammal (the mammal has a condition obtained neovascular commulation in peripheral limbs or in lungs, peritoneal cavity, pleura, cycumulature. The monomeric and bicyclic peptides are used to interfere cyasculature. The monomeric and bicyclic peptides are used to interfere with at least one biological activity induced by VEGF, VEGF-C or -D and chrotic inflammation, especially rheumatoid arthritis, psoriasis and distance of all the combination with an anti-inflammatory agent, to treat a chronic rifflammation, especially rheumatoid arthritis, psoriasis and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SAPHO syndrome, synovitis; acne; pustulosis; hypertosis; osteomyelitis; uveitis; endophthalmitis; bone; joint; central nervous system; ELISA; inflammatory lesion; acne vulgaris; enzyme linked immunosorbent assay; dermatological; osteopathic; neuroprotectant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Propionibacterium acnes polypeptides and nucleic acids useful for vaccinating against and diagnosing infections, especially useful for treating acne vulgaris.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%; Score 42; DB 4; Length 7; 100.0%; Pred. No. 1.4e+06; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Propionibacterium acnes immunogenic protein #23458.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Wang SS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mitcham JL, Wang St
, Jen S, Carter D;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAU62562 standard; protein; 50 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     21-APR-2000; 2000US-0199047P.
02-JUN-2000; 2000US-0208841P.
07-JUL-2000; 2000US-0216747P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    20-APR-2001; 2001WO-US012865.
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L'maisonneuve J, Zhang Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         7; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                       diabetic retinopathy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CVPLTSC 7
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Best Local Similarity
Matches 7; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            N-PSDB; AAS59627
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 7 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      27-FEB-2002
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Sequences AAU39105-AAU68017 represent Propionibacterium acnes immunogenic polypeptides. The proteins and their associated DNA sequences are used in the treatment, prevention and diagnosis of medical conditions caused by the treatment, prevention and diagnosis of medical conditions caused by acnes. The disorders include SAPHO syndrome (synovitis, acne, busulosis, hypertosis and osteomyellitis), uveitis and endophthalmitis. Uservous system, however it is particularly involved in the inflammatory researce or absence of P. acnes in a patient comprises contacting the presence or absence of P. acnes in a patient comprises contacting a presence or absence of P. acnes in a patient comprises contacting a competition and determining the amount of bound protein in the sample. The polypeptides may be used as antigens in the production of antibodies contacting the amount of bound protein in the sample. The competition for a canes proteins. These antibodies and character treat P. acnes proteins. These antibodies and character expression and activity of P. acnes polypeptides and character treat P. acnes infections. The antibodies may also be used as diagnostic agents for determining P. acnes polypeptides and character this patent did not form part of the printed specification, but was for the contained in electronic format directly from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New Propionibacterium acnes polypeptides and polynucleotides encoding the polypeptide, useful for diagnosing, preventing or treating acne vulgaris, or for stimulating an immune response specific for a P. acnes protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Maisonneuve JL;
Jones R, Carter D;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Propionibacterium acnes predicted ORF-encoded polypeptide #23757.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            4; Length 50;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1; Indels
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Benson DR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Example 1; SEQ ID NO 23757; 1481pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 38; DB 4; Pred. No. 38; 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                      ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Persing DH,
Lodes MJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ABM59081 standard; protein; 50 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mitcham JL, Skeiky YAW, Pers:
Zhang Y, Wang S, Jen S, Lodé
Barth B, Vallieve-Douglass J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  15-OCT-2001; 2001US-00978825
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  90.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               11-OCT-2002; 2002WO-US032727
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         6; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2003-381789/36.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                22 CAPLTSC 28
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO2003033515-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 50 AA;
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Novel human diagnostic protein #13161.
                                                                                                                                                                                         ABG13170 standard; protein; 74 AA.
                                                                                                                                                                                                                                                                        30-MAR-2001; 2001WO-US008631.
                                                                                                                                                                                                                                                                                 31-MAR-2000; 2000US-00540217.
23-AUG-2000; 2000US-00649167.
                                                                                                                                 Query Match
Best Local Similarity 85.70,
6; Conservative
                                                                                                                                                                                                            (first entry)
                                                                                                                                                                  22 CAPLTSC 28
                                                                                                                                                                                                                                                                                                         Drmanac RT, Liu C,
                                                                                                                                                        1 CVPLTSC 7
                                                                                                                                                                                                                                                                                               (HYSE-) HYSEQ INC.
                                                                                                                             Sequence 50 AA;
                                                                                                                                                                                                                                                      WO200175067-A2.
                                                                                                                                                                                                            18-FEB-2002
                                                                                                                                                                                                                                            Homo sapiens
                                                                                                                                                                                                                                                              11-OCT-2001.
                                                                                                                                                                                                  ABG13170;
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The invention relates to isolated polymucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polymucleotides are also used in diagnostics as expressed sequence tags for identifying expressed control of (II) are to treat disease states involving (II). (II) is cativity of (II) or to treat disease states involving (II). (II) is useful in tissue, as molecular weight markers and as a food cuplement. (II) and its binding pattners are useful in medical imaging of supplement. (II) and its binding pattners are useful in medical imaging of supplement. (II) and its binding pattners are useful in medical imaging of supplement. (IC) and its binding pattners are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polymucleotide sequences have applications in capporations in the private of data and products dependent on DNA and and to produce other types of data and products dependent on DNA and and confidence other types of the and products dependent on DNA and and acid sequences. ABG00010-ABG30377 represent novel human diagnostic amino acid sequences of the invention. Note: The sequence data for this patent did not appear in the printed specification, but was obtained in correct the produce of the sequences.

The produce of the sequences of the sequence are for this correct or and to produce of the produce of the sequence of the sequence of the sequence of the sequences of the sequence of the sequ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4; Length 74;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human nervous system related polypeptide SEQ ID NO 4699.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1; Mismatches
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Pred. No. 53;
                                             Claim 20; SEQ ID NO 43529; 103pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      90.5%;
85.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        17-JAN-2001; 2001WO-US001334.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 CVPLTSC 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 74 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         04-FEB-2000;
24-FEB-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 31-JAN-2000;
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0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            from WIPO at ftp.wipo.int/pub/published_pct_sequences
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2000US-0186350P. 2000US-0189874P.

02-MAR-2000; 16-MAR-2000;

17-MAR-2000; 2000US-0190076P.

2000US-0198123P. 2000US-0205515P. 2000US-0209467P 2000US-0214886P 2000US-0215135P

19-MAY-2000; 07-JUN-2000; 28-JUN-2000; 30-JUN-2000;

New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess biodiversity.

WPI; 2001-639362/73

N-PSDB; AAS77357

0

Gaps ;

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11.-JUL-2000; 2000US-0216880FF.
14.-JUL-2000; 2000US-02180FF.
14.-JUL-2000; 2000US-02180FF.
14.-JUL-2000; 2000US-02180FF.
14.-JUL-2000; 2000US-022096FF.
14.-JUL-2000; 2000US-022096FF.
14.-JUL-2000; 2000US-022096FF.
14.-JUL-2000; 2000US-022241FF.
14.-JUL-2000; 2000US-022244FF.
14.-JUL-2000; 2000US-022214FF.
14.-JUL-2000; 2000US-022314FF.
14.-JUL-2000; 2000US-022314FF.
14.-JUL-2000; 2000US-022314FF.
14.-JUL-2000; 2000US-022314FF.
14.-JUL-2000; 2000US-022314FF.
14.-JUL-2000; 2000US-022314FF.
15.-JUL-2000; 2000US-02314FF.
16.-SEP-2000; 2000US-02314FF.
17.-SEP-2000; 2000US-02314FF.
18.-SEP-2000; 2000US-02314FF.
19.-SEP-2000; 2000US-02314FF.
11.-SEP-2000; 2000US-02314FF.
11.-SEP-2000; 2000US-02314FF.
11.-SEP-2000; 2000US-02314FF.
12.-SEP-2000; 2000US-02314FF.
13.-SEP-2000; 2000US-02314FF.
14.-SEP-2000; 2000US-02314FF.
15.-SEP-2000; 2000US-02314FF.
16.-SEP-2000; 2000US-02314FF.
17.-SEP-2000; 2000US-02314FF.
18.-SEP-2000; 2000US-02314FF.
19.-SEP-2000; 2000US-02314FF.
19.-SEP-
2000US-0216647P.
2000US-0216880P.
2000US-0217487P.
2000US-0217487P.
2000US-0219829P.
2000US-0229645.
2000US-0229647P.
2000US-0225214P.
2000US-0225214P.
2000US-0225214P.
2000US-0225214P.
2000US-0225214P.
2000US-0225214P.
2000US-0225218P.
2000US-0225268P.
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2000US-02254754P.
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20-OCT-2000; 2000US-0241809P.
20-OCT-2000; 2000US-0241826P.
20-OCT-2000; 2000US-0244617P.
08-NOV-2000; 2000US-0246474P.
08-NOV-2000; 2000US-0246474P.
08-NOV-2000; 2000US-0246476P.
08-NOV-2000; 2000US-0246477P.
08-NOV-2000; 2000US-0246477P.
08-NOV-2000; 2000US-0246477P.
08-NOV-2000; 2000US-0246528P.
08-NOV-2000; 2000US-0249208P.
17-NOV-2000; 2000US-0249218P.
17-NOV-2000; 200US-0249218P.
17-NOV-2000; 2000US-0249218P.
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Rosen CA, Barash SC, Ruben SM (HUMA-) HUMAN GENOME SCI INC

WPI; 2001-541565/60. N-PSDB; ABA12368.

Nucleic acids encoding 3224 human nervous system antigen polypeptides, useful for preventing, diagnosing and/or treating nervous system cancers and metastases.

Claim 11; SEQ ID NO 4699; 1701pp + Sequence Listing; English.

The invention relates to novel genes (ABA11004-ABA21534) and proteins (ABB14678-ABB18001) useful for preventing, treating or ameliorating medical conditions e.g. by protein or gene therapy. The genes are isolated from a range of human tissues disclosed in the specification. The nucleic acids, proteins, antibodies and (ant) agonists are useful in the diagnosis, treatment and prevention of: (a) cancer, e.g. breast and ovarian cancer and other cancers of the adrenal gland, bone, bone marrow,

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27-FEB-2002
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breast, gastrointestinal tract, liver, lung, or urogenital; (b) immune disorders e.g. Addison's disease, allergies, autoimmune haemolytic anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's disease, multiple sclerosis, rheumatoid arthritis and ulcerative colitis; (c) cardiovascular disorders such as myocardial ischaemias; (d) wound healing; (e) neurological diseases e.g. cerebral anoxia and epilepsy; and (f) infectious diseases such as viral, bacterial, fungal and parasitic infections. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences .; 0 Sequences AAU39105-AAU68017 represent Propionibacterium acnes immunogenic polypeptides. The proteins and their associated DNA sequences are used in the treatment, prevention and diagnosis of medical conditions caused by P. acnes. The disorders include SAPHO syndrome (synovitis, acne) pustulosis, hypertosis and osteomyelitis), uveitis and endophthalmitis. P. acnes is also involved in infections of bone, joints and the central nervous system, however it is particularly involved in the inflammatory lesions associated with acne vulgaris. A method for detecting the presence or absence of P. acnes in a patient comprises contacting a sample with a binding agent that binds to the proteins of the invention SAPHO syndrome; synovitis; acne; pustulosis; hypertosis; osteomyelitis; uveitis; endophthalmitis; bone; joint; central nervous system; ELISA; inflammatory lesion; acne vulgaris; enzyme linked immunosorbent assay; dermatological; osteopathic; neuroprotectant. Gaps Propionibacterium acnes polypeptides and nucleic acids useful for vaccinating against and diagnosing infections, especially useful for 0; Bhatia A; DB 4; Length 64; 68; 1; Indels Propionibacterium acnes immunogenic protein #25135. Wang SS, Mitcham JL, Wang S., Jen S, Carter D; Score 37; DB 4 Pred. No. 68; 0; Mismatches Example 1; SEQ ID NO 25434; 1069pp; English. AAU64239 standard; protein; 91 AA. , 88.1%; 21-APR-2000; 2000US-0199047P. 02-JUN-2000; 2000US-0208841P. 07-JUL-2000; 2000US-0216747P. 20-APR-2001; 2001WO-US012865. Skeiky YAW, Persing DH, M L'maisonneuve J, Zhang Y, (first entry) Local Similarity 85.7 Propionibacterium acnes. treating acne vulgaris. 28 CXPLTSC 34 WPI; 2001-616774/71. 7 (CORI-) CORIXA CORP. 1 CVPLTSC N-PSDB; AAS59641 Sequence 64 AA; WO200181581-A2

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The invention relates to an isolated polynucleotide (ACF64435-ACF64733) encoding a Propionibacterium acnes protein. The invention also relates to polypeptides encoded by the polynucleotides (ABMS624-ABM64536) and to additionally encompasses expression vectors and host cells comprising a polyputaleotide of the invention; antibodies against polypeptides of the invention; antibodies against polypeptides of the invention; antibodies against polypeptides of the invention; an immune response specific for a P. acnes polypeptide and an isolated T cell population comprising T cells prepared via this method; a vaccine composition (comprising P. acnes polypeptides, polymucleotides, antibodies, fusion proteins, T cell populations, or antigen-presenting cells that express the polypeptide); a method and kit for detecting or determining the presence or absence of P. acnes in a
and determining the amount of bound protein in the sample. The polypeptides may be used as antigens in the production of antibodies specific for practise. These antibodies can be used to downregulate expression and activity of P. acnes polypeptides and therefore treat P. acnes infections. The antibodies may also be used as diagnostic agents for determining P. acnes presence, for example, by enzyme linked immunosorbent assay (ELISA). Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           polypeptide, useful for diagnosing, preventing or treating acne vulgaris, or for stimulating an immune response specific for a P. acnes protein.
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Jones R, Carter D;
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Pred. No. 1.4e+02;
); Mismatches 1; Indels
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Lodes MJ, Benson DR,
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Zhang Y, Wang S, Jen S, Lode
Barth B, Vallieve-Douglass J;
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85.7%;
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patient; and a method for inhibiting the development of P. acnes in a patient. The P. acnes polypeptides, polynucleotides, antibodies, fusion proteins, T cell populations or antigen-presenting cells that express the colypeptides are useful for diagnosing, preventing or treating acne ulgaris, or for stimulating an immune response specific for a P. acnes protein. The polynucleotides can also be used as probes or primers for nucleic acid hybridisation. The vaccine composition is useful for the stimulation of an immune response against P. acnes, or for treating acne, and the kit is useful for performing a diagnostic assay. The present and the kit is useful for performing a diagnostic assay. The present cading frame) contained within the P. acnes polynucleotides of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences 85.7%; 6; Conservative Query Match Best Local Similarity Sequence 91 AA; Matches 8x88888888888888888

Length 91; 1; Indels Score 36; DB 6; I Pred. No. 1.4e+02; 0; Mismatches 75 CVPRTSC 81 1 CVPLTSC 7 ò

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RESULT

ABG30203 standard; protein; 4561 AA ABG30203; Novel human diagnostic protein #30194.

(first entry)

18-FEB-2002

Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder.

Homc sapiens.

WO200175067-A2.

11-CCT-2001.

30-MAR-2001; 2001WO-US008631.

31-MAR-2000; 2000US-00540217. 23-AUG-2000; 2000US-00649167.

HYSE-) HYSEQ INC

Tang YT; Drmanac RT, Liu C,

WPI; 2001-639362/73 N-PSDB; AAS94390 New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess biodiversity

claim 20; SEQ ID NO 60562; 103pp; English.

The invention relates to isolated polymucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oilgomers, and for chromosome and gene mapping, and in recombinant production of (II). The polymucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food

The invention relates to isolated polymucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polymucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders 0 supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for traating disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleoride sequences have applications in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and amino acid sequences. ABG00010-ABG30377 represent novel human diagnostic amino acid sequences of the invention. Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences Gaps New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder. 0 Score 36; DB 4; Length 4561; Pred. No. 4.4e+03; 2; Mismatches 0; Indels Claim 20; SEQ ID NO 51423; 103pp; English. Novel human diagnostic protein #21055. ABG21064 standard; protein; 9222 AA. 2; 30-MAR-2001; 2001WO-US008631. 31-MAR-2000; 2000US-00540217. Tang YT; 23-AUG-2000; 2000US-00649167 85.7%; 71.4%; (first entry) Conservative 2931 CVPISSC 2937 WPI; 2001-639362/73 Liu C, Best_Local Similarity Matches 5; Conserv 1 CVPLTSC 7 HYSE-) HYSEQ INC. N-PSDB; AAS85251 Sequence 4561 AA; WO200175067-A2. Homo sapiens. biodiversity 18-FEB-2002 Drmanac RT, 11-0CT-2001 ABG21064; Query Match RESULT 9 ABG21064 qq ò

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2000US-0227009P
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2000US-0229343P
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involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and amino acid sequences. ABG00010-ABG30377 represent novel human diagnostic patent did not appear in the printed specification, but was obtained in ftp.wipo.int/pub/published_pot_sequences
                                                                                                                                                                                                                                                                                                                                     Human; reproductive system related antigen; reproductive system disorder; cancer; gene therapy.
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                                                                                                                                       85.7%; Score 36; DB 4; Length 9222; 71.4%; Pred. No. 8.2e+03;
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24-FEB-2000; 2000US-0186628P.
22-MAR-2000; 2000US-0186350P.
16-MAR-2000; 2000US-0189374P.
17-MAR-2000; 2000US-0189374P.
17-MAR-2000; 2000US-0199076P.
18-APR-2000; 2000US-0199076P.
19-MAY-2000; 2000US-020515P.
28-JUN-2000; 2000US-021513P.
28-JUN-2000; 2000US-021513F.
30-JUN-2000; 2000US-0215486P.
30-JUN-2000; 2000US-0217487P.
11-JUL-2000; 2000US-0217496P.
11-JUL-2000; 2000US-0217496P.
11-JUL-2000; 2000US-0218290P.
26-JUL-2000; 2000US-0218290P.
26-JUL-2000; 2000US-0218290P.
26-JUL-2000; 2000US-0221829P.
14-AUG-2000; 2000US-022518P.
14-AUG-2000; 2000US-0225218P.
14-AUG-2000; 2000US-0225218P.
14-AUG-2000; 2000US-0225266P.
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reproductive system disorder; urinary system disorder; gene therapy; cardiovascular disorder; respiratory disorder; neurological disorder; gastrointestinal disease; infection; cytostatic.
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21-SEP-2000;
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14-AUG-2000;
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30-AUG-2000;
                                                                          Homo sapiens
                                                                                                                                         02-AUG-2001
        Isolated nucleic acid molecule encoding a reproductive system antigen is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present invention provides the protein and coding sequences of a number of human reproductive system related antigens. These can be used in the prevention and treatment of reproductive system disorders, including cancer. The present sequence is a protein of the invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 11; SEQ ID NO 5223; 1297pp + Sequence Listing; English.
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N-PSDB; AAL02535.
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11-DEC-2000;
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17-NOV-2000;
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Matches 6;
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2000US-0251989P.
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13-OCT-2000; 20
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02-OCT-2000; 2
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17-NOV-2000;
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antianaemic; dermatological; immunosupressive, antiinflammatory; antianfmitic; antirheumatic; virucide; hepatotropic; nephrotropic; osteopathic; prostate gland; prostatitis; adenocarcinoma; hair loss; prostatosis; malacoplakia; adenocarcinoma; benign prostatic hypertrophy; hyperplasia; carcinoma; prostate neoplastic disorder; skin aging; reproductive system disorder; autoimmune disorder; skin aging; system; lupus erythematosus; rheumatoid arthritis; cardiovascular; blood-related disorder; hyperproliferative disorder; respiratory; neurological disorder; endocrine disorder; inflammatory disorder; liver disorder; wound healing; food preservative.

2000US-0190076P. 2000US-0198123P. 2000US-0205515P. 2000US-0209467P.

19-MAY-2000; 07-JUN-2000;

28-JUN-2000;

2000US-0214886P

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04-FEB-2000; 2000US-0180628P. 24-FEB-2000; 2000US-0184664P. 02-MAR-2000; 2000US-0186350P.

2000US-0179065P

31-JAN-2000;

17-JAN-2001; 2001WO-US001330.

WO200155447-A1 Homo sapiens

02-AUG-2001

Human, nootropic, neuroprotective, cytostatic, antiparkinsonian,

Novel prostate gland antigen, Seq ID No 158.

(first entry)

21-NOV-2001

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The present invention provides the protein and coding sequences of 973 muman testicular antigens, and fragments of their genomic sequences. The sequences can be used in the treatment of cardiovascular, urinary system, reproductive system, immune, respiratory, neurological and system, gastrointestinal disorders, infections, and particularly cancer, especially testicular cancers. The present sequence is a protein of the
                                                                                         Nucleic acids encoding 973 human testicular antigen polypeptides, useful for preventing, diagnosing and/or treating testicular cancer.
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85.7%; Pred. No. 1.4e+02;
ive 0; Mismatches 1; Indels
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                                                                                                                        Claim 11; SEQ ID NO 1953; 766pp; English.
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                                                    Ruben SM;
11-DEC-2000; 2000US-0254097P.
05-JAN-2001; 2001US-0259678P.
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Matches 6; Conservative
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                                                                       WPI; 2001-483232/52.
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30-JUN-2000; 2000US-0215135P.
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07-JUL-2000; 2000US-021748FP.
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17-NOV-2000;
17-NOV-2000;
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(HUMA-) HUMAN GENOME SCI INC

Rosen CA, Barash SC,

WPI; 2001-476223/51. N-PSDB; AAS30300.

Novel isolated prostate gland related polypeptide useful for diagnosis and treatment of disorders of prostate such as prostatodystonia, prostatosis, prostatitis, benign prostatic hypertrophy and malacoplakia

Claim 1; SEQ ID NO 158; 512pp; English.

The invention relates to novel isolated prostate gland related nucleic acids (I) and polypeptides (II). (I) and (II) are useful for diagnosis, prognosis, prevention, and/or treatment of diseases and/or disorders of the prostate such as acute non-bacterial prostatitis, chronic non-bacterial prostatitis, prostatodystonia, prostatosis, granulomatous prostatitis, malacoplakia, benign prostatic

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              hypertrophy or hyperplasia, and prostate neoplastic disorders, including adenocarcinomas, transitional cell carcinomas, ductal carcinomas, and squamous cell carcinomas. [1], (II) and antibody to (II) are useful for diagnosing and treating reproductive system disorders (Paget's disease), autoimmune disorders (systemic lupus erythematosus, rheumatoid autoimmune disorders (systemic lupus erythematosus, rheumatoid hyperproliferative disorders, urinary system disorders (sickle cell anaemia), hyperproliferative disorders, urinary system disorders (arrhythmias), respiratory conflowascular disorders (arrhythmiss), respiratory cardiovascular disorders (arrhythmisson's disease), condocrine disorders (Alzhemmer's disease) and Parkinson's disease), condocrine disorders (Alzhemmer's disorders (biliary liver cirrhosis), pancreatic and gall bladder disorders (biliary liver cirrhosis), pancreatic and gall bladder disorders, disorders of the large intestine, developmental and inherited disorders, disorders of the callular level, and wound healing and epithelial cell proliferation. (I) or (II) is useful to prevent skin aging, for preventing hair loss, to maintain
                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human; reproductive system related antigen; reproductive system disorder; cancer; gene therapy.
                                                                                                                                                                                                                                               Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                            Human reproductive system related antigen SEQ ID NO: 3611.
                                                                                                                                                                                                             Ouery Match
83.3%; Score 35; DB 4; Length 65;
Best Local Similarity 71.4%; Pred. No. 1.5e+02;
Matches 5; Conservative 2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                    AAM94953 standard; protein; 65 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  04-FEB-2000; 2000US-01806628P.
24-FEB-2000; 2000US-0184664P.
02-MAR-2000; 2000US-0184664P.
16-MAR-2000; 2000US-018913-0.
19-MAR-2000; 2000US-0199123-0.
19-MAY-2000; 2000US-0199123-0.
19-MAY-2000; 2000US-0205467P.
28-JUN-2000; 2000US-0215135-0.
28-JUN-2000; 2000US-0215135-0.
30-JUN-2000; 2000US-0215135-0.
11-JUL-2000; 2000US-0216880P.
11-JUL-2000; 2000US-0217487P.
11-JUL-2000; 2000US-0217487P.
11-JUL-2000; 2000US-0217487P.
11-JUL-2000; 2000US-0217487P.
26-JUL-2000; 2000US-0217487P.
26-JUL-2000; 2000US-0217487P.
26-JUL-2000; 2000US-0217487P.
26-JUL-2000; 2000US-0217487P.
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2000US-0225213P.
2000US-0225214P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2000US-0225267P.
2000US-0225268P.
2000US-0225270P.
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                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
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CLPLSSC 47
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14-AUG-2000; 2
14-AUG-2000; 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        31-JAN-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     14-AUG-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        02-AUG-2001
                                                                                                                                                                                                                                                                                                                                                                             AAM94953;
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Propionibacterium acnes immunogenic protein #9908.
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                                                                                                                                                                                                                                                                                                                                                                                                  Isolated nucleic acid molecule encoding a reproductive system antigen is used in preventing, treating or ameliorating a medical condition.
                                                                                                                                                                                                                                                                                                                                                                                                                                             The present invention provides the protein and coding sequences of a number of human reproductive system related antigens. These can be used in the prevention and treatment of reproductive system disorders, including cancer. The present sequence is a protein of the invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity 71.4%; Score 35; DB 4; Length 65; Similarity 71.4%; Pred. No. 1.5e+02; 5; Conservative 2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAU49012 standard; protein; 80 AA.
                                                                                                                                                                                                                                                                                                                                                           Ruben SM;
           2000US-0246609P.
2000US-0246610P.
2000US-0246613P.
2000US-0249207P.
2000US-0249209P.
2000US-0249210P.
2000US-0249210P.
2000US-0249211P.
2000US-0249213P.
2000US-0249213P.
2000US-0249213P.
2000US-0249213P.
                                                                                                                                                                    2000US-0249264P.
2000US-0249265P.
2000US-0249297P.
                                                                                                                                                                                                                                                                                                                                         (HUMA-) HUMAN GENOME SCI INC.
                                                                                                                          2000US-0249216P.
2000US-0249217P.
2000US-0249218P.
                                                                                                                                                                                                               2000US-0250160P.
                                                                                                                                                    2000US-0249244P.
2000US-0249245P.
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2000US-0249300P.
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                                                                                                                                                                                                                                                                             2000US-025186BP
                                                                                                                                                                                                                                                                                     08-DEC-2000; 2000US-0251869P
                                                                                                                                                                                                                                                                                                      2000US-0251990P
                                                                                                                                                                                                                                                                                                                       05-JAN-2001; 2001US-0259678P
                                                                                                                                                                                                                                                            2000US-0251479P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            27-FEB-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                           Barash SC,
                                                                                                                                                                                                                                                                                                                                                                            WPI: 2001-465570/50.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         |:||:||
CLPLSSC 47
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                      N-PSDB; AAL00923
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 65 AA;
                                                                                                                                                                                                                        01-DBC-2000)
05-DBC-2000)
05-DBC-2000)
05-DBC-2000)
06-DBC-2000)
08-DBC-2000)
08-DBC-2000)
                                                                                                 17-NOV-2000;
17-NOV-2000;
17-NOV-2000;
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                                     08-NOV-2000;
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17-NOV-2000;
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17-NOV-2000;
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17-NOV-2000;
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                              38-NOV-2000;
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polypeptides. The proteins and their associated DNA sequences are used in the treatment, prevention and diagnosis of medical conditions caused by the treatment, prevention and diagnosis of medical conditions caused by a cnes. The disorders include SAPHO syndrowitis, acre, p. acnes. The disorders include SAPHO syndrowitis, acre, p. acnes is also involved in infections of bone, joints and the central nervous system, however it is particularly involved in the inflammatory resence or absence of P. acnes in a partient comprises contacting a sample with a binding agent that binds to the proteins of the invention and determining the amount of bound protein in the sample. The polypeptides may be used as antigens in the production of antibodies of specific for P. acnes proteins. These antibodies can be used as downregulate expression and activity of P. acnes polypeptides and activity of P. acnes presence of the reample of the protein in the sequence data for therefore treat P. acnes infections. The antibodies may also be used as diagnostic agents for determining P. acnes presence. for example, by charmed immunosorbent assay (ELISA). Note: The sequence data for this patent did not form part of the printed specification, but was the content of the printed specification, but was
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequences AAU39105-AAU68017 represent Propionibacterium acnes immunogenic
SAPHO syndrome; synovitis; acne; pustulosis; hypertosis; osteomyelitis; uveitis; endophthalmitis; bone; joint; central nervous system; ELISA; inflammatory lesion; acne vulgaris; enzyme linked immunosorbent assay; dermatological; osteopathic; neuroprotectant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Propionibacterium acnes polypeptides and nucleic acids useful for vaccinating against and diagnosing infections, especially useful for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ..
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 35; DB 4; Length 80;
Pred. No. 1.8e+02;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mitcham JL, Wang SS,
Jen S, Carter D;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Example 1; SEQ ID NO 10207; 1069pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Etp.wipo.int/pub/published_pct_sequences
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         21-APR-2000; 2000US-0199047P.
02-JUN-2000; 2000US-0208841P.
07-JUL-2000; 2000US-0216747P.
                                                                                                                                                                                                                                                                                                                                                                                                                        20-APR-2001; 2001WO-US012865.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Persing DH, M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 85...
G; Conservative
                                                                                                                                                                                                            Propionibacterium acnes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          treating acne vulgaris.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    37 CDPLTSC 43
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (CORI-) CORIXA CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           N-PSDB; AAS59543.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               L'maisonneuve J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 80 AA;
                                                                                                                                                                                                                                                                             WO200181581-A2.
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                                                                                                                                                                                                                                                                                                                                                      01-NOV-2001.
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The invention relates to an isolated polynucleotide (ACF64435-ACF64733) encoding a Propionibacterium acnes protein. The invention also relates to encoded by the polynucleotides (ABM35624-ABM64536) and to immunogenic fragments of P. acnes polypeptides. The invention additionally encompasses expression vectors and host cells comprising a additionally encompasses expression vectors and host cells comprising a colympletide of the invention; antibodies against polypeptides of the invention; tuston proteins comprising a polypeptide of the invention; a method for stimulating an immune response specific for a P. acnes

CC polymucleotides, antibodies, fusion proteins, T cell populations, or contigen-presenting cells that express the polypeptide); a method and kit for detecting or determining the presence of P. acnes in a patient; and a method for inhibiting the development of P. acnes in a patient; and a method for inhibiting the development of P. acnes in a proteins. T cell populations or antigen-presenting cells that express the polypeptides, polypucleides, antiponent of P. acnes in a proteins, T cell populations or antigen-presenting cells that express the volypeptides are useful for diagnosing, preventing or treating acne volgaris, or for stimulating an immune response specific for a P. acnes or primers for nucleic acid hybridisation. The vaccine composition is useful for the stimulation of an immune response against P. acnes, or for treating acne, cand the kit is useful for performing a diagnostic assay. The present cand the kit is useful for performing a diagnostic assay. The present cand the kit is useful for performing a diagnostic assay. The present cand the kit is useful for performing a diagnostic assay. The present cand the kit is useful for performing a diagnostic assay. The present cand the kit is useful to this patent did not form part of invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly and the printed specifi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New Propionibacterium acmes polypeptides and polymucleotides encoding the polypeptide, useful for diagnosing, preventing or treating acme vulgaris, or for stimulating an immune response specific for a P. acmes protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Maisonneuve JL;
Jones R, Carter D;
                       Propionibacterium acnes predicted ORF-encoded polypeptide #10207.
                                                                          Acne vulgaris; antiseborrhoeic; dermatological; antibacterial; immunostimulant; immune response; vaccine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bhatia A,
Benson DR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Example 1; SEQ ID NO 10207; 1481pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mitcham JL, Skeiky YAW, Persing DH,
Zhang Y, Wang S, Jen S, Lodes MJ,
Barth B, Vallieve-Douglass J;
                                                                                                                                                                                                                                                                                                       11-OCT-2002; 2002WO-US032727.
                                                                                                                                                                                                                                                                                                                                                         15-OCT-2001; 2001US-00978825.
                                                                                                                                                    Propionibacterium acnes.
                                                                                                                                                                                                                                                                                                                                                                                                            (CORI-) CORIXA CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2003-381789/36.
N-PSDB; ACF64472.
                                                                                                                                                                                                       WO2003033515-A1
                                                                                                                                                                                                                                                         24-APR-2003
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Sequence 80 AA;

Gaps . 0 83.3%; Score 35; DB 6; Length 80; 85.7%; Pred. No. 1.8e+02; ive 0; Mismatches 1; Indels Query Match Best Local Similarity 85.7°, Best Gonservative à

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Search completed: September 5, 2004, 09:55:17 Job time: 25.9798 secs

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Sequence Sequence Sequence

Sequence 3546, Appliage Sequence 2, Appliage Sequence 1243, Appliage Sequence 1243, Appliage Sequence 465, Appliage Sequence 20, Appliage Sequence 4, Appliage Sequence 2, Appliage Sequence 1116, Appliage Sequence 148382, Sequence 158802, Sequence 158802, Sequence 158802, Sequence 215673, Sequence 215673, Appliage Sequence 158802, Sequence 158802, Sequence 215673, Appliage Sequence 215673, Appliage Sequence 158802, Sequence 215673, Appliage Sequence 215673, Appliage

Sequence 46, Appl Sequence 8827, Ap Sequence 8828, Ap Sequence 104490,

Sequence 32138, A Sequence 33904, A Sequence 219, App

Title: Perfect score:

Sequence:

Scoring table:

Searched:

Database

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APPLICANT: ACHEN, Marc
APPLICANT: STACKER, Steven
APPLICANT: HUGHES, Richard
APPLICANT: HUGHES, Richard
APPLICANT: HUGHES, Richard
APPLICANT: CENDRON, Angela
TITLE OF INVENTION: VEGF-D/VEGF-C/VEGF PEPTIDOMIMETIC INHIBITOR
FILE REPREBRUCE: 1064/48505 Achen et al
CURRENT APPLICATION NUMBER: 0209/761,636A
CURRENT FILING DATE: 2001-01-18
PRIOR FILING DATE: 2000-01-18
PRIOR FILING DATE: 2000-01-18
PRIOR FILING DATE: 2000-05-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100.0%; Score 42; DB 9; Length 7; ilarity 100.0%; Pred. No. 1.2e+06; Conservative 0; Mismatches 0; Indels
4 US-10-120-018-12

US-10-263-929-116

US-10-120-018-9

US-10-108-260A-3546

US-10-108-260A-3546

US-10-112-944-465

US-10-112-944-465

US-10-029-386-29056

US-10-112-944-465

US-10-112-948-4

US-10-112-948-4

US-10-112-94-199-1189382

US-10-28-115-7-18-2

US-10-28-115-7-18-2

US-10-424-599-1189382

US-10-424-599-1189323

US-10-424-599-1189382

US-10-424-599-1189382

US-10-424-599-1189382

US-10-437-963-104490

US-10-335-977-8828

US-10-335-977-8828

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US-10-335-977-8828
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-10-424-599-248060
; Sequence 248060, Application US/10424599
; Publication No. US20040031072A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-761-636A-11
; Sequence 11, Application US/09761636A
; Patent No. US20020065218A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQ ID NOS: 34
SOFTWARE: PatentIn version 3.0
  ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
Matches 7; Conserv
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  CVPLTSC
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    SEQ ID NO 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT
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  à
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Sequence 3611, Ap
Sequence 5, Appli
Sequence 1832, Ap
Sequence 48, Appl
Sequence 1835, Ap
Sequence 1835, Ap
Sequence 58, Appl
Sequence 16, Appl
Sequence 16, Appl
Sequence 16, Appl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 11, Appl
Sequence 248060,
Sequence 199668,
Sequence 118478,
                                                                                             September 5, 2004, 10:00:15; Search time 19.6566 Seconds (without alignments) 112.199 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep:*
2: /cgn2_6/ptodata/2/pubpaa/PCT_MBW_PUB_pep:*
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9: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
11: /cgn2_6/ptodata/2/pubpaa/US09E_PUBCOMB.pep:*
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12: /cgn2_6/ptodata/2/pubpaa/US108_PUBCOMB.pep:*
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18: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep:*
             GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-09-764-891-5223
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US-09-764-891-5213
US-10-120-0118-5
US-10-091-458-48
US-10-191-254-48
US-09-813-245-1835
US-10-016-248-58
US-10-120-018-16
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Gaps

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Result Š. 0;

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TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement FILE REFERENCE: 38-21(5321)B
CURRENT APPLICATION NUMBER: US/10/437,963
CURRENT FILING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
SEQ ID NO 118478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids NAME/KEY: SITE LOCATION: (60)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids US-09-764-891-5223
                                                                                                                                                                                                                                                                                                                                                                      Gaps
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; Sequence 361, Application US/09764891
; Publication No. US20030077808A1
; GENERAL INFORMATION:
; APPLICAMY: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; TITLE OF INVENTION NUMBER: US/09/764,891
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 10231
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3611
; LENGTH: 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 5223, Application US/09764891
; Publication No. US20030077808A1
; GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PC006
CURRENT APPLICATION NUMBER: US/09/764,891
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 10231
; SOFTWARE: Patentin Ver. 2.0
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US-10-437-963-118478
                                                                                                                                                                                                                                                                                                                        16;
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Pred. No. 66;
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71.4%;
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Best Local Similarity 71.4
Matches 5, Conservative
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ORGANISM: Oryza sativa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT
ORGANISM: Homo sapiens
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LOCATION: (58)
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US-09-764-891-3611
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                    APPLICANT: La Rosa Thomas J
APPLICANT: La Rosa Thomas J
APPLICANT: La Rosa Thomas J
APPLICANT: About K
APPLICANT: About Vibra
APPLICANT: About Vibra
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53223) B
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
ENGTH: 118
LENGTH: 118
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Pred. No. 46;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1; Indels
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US-10-424-599-199668
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Sequence 118478, Application US/10437963

Publication No. US2040123343A1

GENERAL INFORMATION:

APPLICANT: La Rosa, Thomas J.

APPLICANT: Kovalic, David K.

APPLICANT: Cao, Yongwei

APPLICANT: Wu, Wei
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Publication No. US20040031072A1
GENERAL INFORMATION:
APPLICANT: La Rosa Thomas J
APPLICANT: Kovalic David K
APPLICANT: Zhou Yihua
APPLICANT: Cao Yongwei
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Barbazuk, Brad
Li, Ping
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85.7%;
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Best Local Similarity 85.7
Matches 6; Conservative
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ORGANISM: Glycine max
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Best Local Similarity
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OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
NAME/KEY: SITE
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OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
NAME/KEY: SITE
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OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
                                                                                                                                                                                                                                                                                    | Sequence 5, Application US/10120018
| Sequence 5, Application US/10120018
| Publication No. US20030194708A1
| GENERAL INFORMATION:
| APPLICAMT: Binnerts et al
| TITLE OF INVENTION: Human Homolog of Crossveinless Materials and Methods
| FILE REFERENCE: 28110/37995
| CURRENT APPLICATION NUMBER: US/10/120,018
| CURRENT FILING DATE: 2002-04-10
| NUMBER OF SEQ ID NOS: 17
| SOFTWARE: PatentIn version 3.0
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Pred. No. 2.3e+02;
3; Mismatches 0; Indels
                                                                                Score 35; DB 10; Length 65; Pred. No. 86;
                                                                                                                            0; Indels
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Publication No. US20040010134A1
GENERAL INFORMATION:
APPLICANT: Human Genome Sciences, Inc.
TITLE OF INVENTION: Albumin Fusion Proteins
FILE REPERENCE: PF946CT
CURRENT APPLICATION NUMBER: 05/09/833,245
CURRENT FILING DATE: 2001-04-12
PRIOR PLING DATE: 2000-04-12
PRIOR PLING DATE: 2000-04-12
PRIOR PLING DATE: 2000-12-21
PRIOR APPLICATION NUMBER: 60/256, 931
PRIOR PLING DATE: 2000-12-21
PRIOR APPLICATION NUMBER: 60/199, 384
PRIOR FILING DATE: 2000-04-25
NUMBER OF SEQ ID NOS: 2267
SOFTWARE: PALENTING DATE: 2000-04-25
NUMBER OF SEQ ID NOS: 2267
SEQ ID NO 1832
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Best Local Similarity 71.4%;
Matches 5; Conservative
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ORGANISM: Homo sapiens
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-764-891-3611
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; ORGANISM: Homo sapiens
US-10-120-018-5
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41 CLPLSSC 47
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50 CIPISSC 56
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Best Local Similarity
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NAME/KEY: SITE
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US-09-833-245-1832
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LENGTH: 19
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RE: 60/241,809 -10-20 -11-27 -11-17 -17-29 -11-17 -17-29 -18: 60/249,299 -18: 60/243,327 -10-20 -11-01 -11-	112-08 112-08 112-08 112-08 12-08 12-08 13	10-02 11-02 11-02 11-02 11-02 11-02 11-02 11-02 11-02 11-02 11-03 11
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R APPLICATION NUMBER: 60/235, 836
R FILING DATE: 2000-09-27
R FILING DATE: 2000-09-06
R FILING DATE: 2000-09-06
R APPLICATION NUMBER: 60/215, 135
R FILING PATE: 2000-06-30
R FILING PATE: 2000-06-30
R FILING DATE: 2000-08-14
R FILING DATE: 2000-08-14
R APPLICATION NUMBER: 60/25, 266
R FILING DATE: 2000-08-14 R APPLICATION NUMBER: 60/232,080
R FILING DATE: 2000-09-08
R APPLICATION NUMBER: 60/231,414
R FILING DATE: 2000-09-08
R APPLICATION NUMBER: 60/231,244
R FILING DATE: 2000-09-08 FILING DATE: 2000-11-17
APPLICATION NUMBER: 60/249,208
FILING DATE: 2000-11-17 FILING DATE: 2000-11-17 APPLICATION NUMBER: 60/249,212 FILING DATE: 2000-11-17 APPLICATION NUMBER: 60/249,245 FILING DATE: 2000-11-17 APPLICATION NUMBER: 60/249,217 FILING DATE: 2000-11-17 APPLICATION NUMBER: 60/249,211 FILING DATE: 2000-11-17 APPLICATION NUMBER: 60/249,215 FILING DATE: 2000-11-17 APPLICATION NUMBER: 60/249,264 FILING DATE: 2000-11-17 FILING DATE: 2000-11-17
APPLICATION UNMBER: 60/232,400
ALLING DATE: 2000-09-14
APPLICATION NUMBER: 60/231,242 APPLICATION NUMBER: 60/233,064 FILING DATE: 2000-09-14 APPLICATION NUMBER: 60/233,063 PILING DATE: 2000-10-20
APPLICATION NUMBER: 60/246,475
PILING DATE: 2000-11-08
APPLICATION NUMBER: 60/231,243
FILING DATE: 2000-09-08 APPLICATION NUMBER: 60/249,213 APPLICATION NUMBER: 60/249,207 FILING DATE: 2000-11-17 APPLICATION NUMBER: 60/249,244 APPLICATION NUMBER: 60/249,214 FILING DATE: 2000-11-17 APPLICATION NUMBER: 60/249,297 FILING DATE: 2000-09-08 APPLICATION NUMBER: 60/232,081 FILING DATE: 2000-09-14 APPLICATION NUMBER: 60/232,397 FILING DATE: 2000-09-14
APPLICATION NUMBER: 60/232,399 APPLICATION NUMBER: 60/232,401 FILING DATE: 2000-09-14 APPLICATION NUMBER: 60/241,808 60/241,826 APPLICATION NUMBER: 60/241,786 FILING DATE: 2000-10-20 APPLICATION NUMBER: 60/241,221 2000-09-08 2000-10-20 2000-10-20 2000-09-14 APPLICATION NUMBER: FILING DATE: 2000-10 FILING DATE: FILING DATE: FILING DATE: FILING DATE: PRIOR PRIOR

Query Match 83.3%; Score 35; DB 14; Length 270; Best Local Similarity 57.1%; Pred. No. 3.16+02; Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps

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LOCATION: (288)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
NAME/KEY: SITE
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OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
NAME/KEY: SITE
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OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
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OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
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TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same FILE REFERENCE: 21402-218
CURRENT APPLICATION WUMBER: US/10/016,248
CURRENT FILING DATE: 2002-09-20
GENERAL INFORMATION:
APPLICANT: Human Genome Sciences, Inc.
TITLE OF INVENTION: Albumin Fusion Proteins
FILE REFERENCE: PF546PCT
CURRENT APPLICATION NUMBER: US/09/833,245
CURRENT FILING DATE: 2001-04-12
PRIOR APPLICATION NUMBER: 60/229, 358
PRIOR FILING DATE: 2000-04-12
PRIOR FILING DATE: 2000-04-12
PRIOR FILING DATE: 2000-12-11
SPRIOR FILING DATE: 2000-04-25
NUMBER OF SEQ ID NOS: 2267
SOFTWARE: PATENTIN Ver. 2.1
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PRIOR APPLICATION NUMBER: 60/254,329
PRIOR FILING DATE: 2000-12-08
PRIOR FILING DATE: 2001-05-15
PRIOR APPLICATION NUMBER: 60/291,037
PRIOR FILING DATE: 2001-05-15
PRIOR FILING DATE: 2000-12-14
PRIOR FILING DATE: 2000-16-18
PRIOR APPLICATION NUMBER: 60/297,173
PRIOR FILING DATE: 2001-06-38
PRIOR PRIOR FILING DATE: 2001-07-31
PRIOR FILING DATE: 2001-07-31
PRIOR FILING DATE: 2001-00-01
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Publication No. US20040033491A1
GENERAL INFORMATION:
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Matches 4; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: SITE
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OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
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                                                                                                                                                                                                                                                        US-10-191-254-48

Dublication No. US200400056501

Sequence 48, Application US/10191254

Publication No. US200400056501

SEGNERAL INFORMATION:

TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies

FILE REPERENCE:

CURRENT FILING DATE: 2002-08-27

PRIOR APPLICATION NUMBER: 10/91,458

PRIOR PELING DATE: 2000-03-01

PRIOR APPLICATION NUMBER: 09/764,900

PRIOR APPLICATION NUMBER: 00/10-1

PRIOR APPLICATION NUMBER: 60/10,628

PRIOR APPLICATION NUMBER: 60/119,665

PRIOR PILING DATE: 2000-01-01

PRIOR APPLICATION NUMBER: 60/214,886

PRIOR FILING DATE: 2000-05-04

PRIOR PAPLICATION NUMBER: 60/225,758

PRIOR PILING DATE: 2000-07-01

PRIOR PAPLICATION NUMBER: 60/225,447

PRIOR PILING DATE: 2000-07-01

PRIOR PILING DATE: 2000-08-14

PRIOR PILING DATE: 2000-08-14
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Best Local Similarity 57.1
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FEATURE:
NAME/KEY: misc feature
LOCATION: (113)
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161 CIPISSC 167
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NUMBER OF SEQ ID NOS: 167 SOFTWARE: Patentin Ver. 2.1 SEQ ID NO 58

; Sequence 1835, Application US/09833245

RESULT 11 US-09-833-245-1835

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RESULT 15
US-10-451-417-4
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                                                                                                                                                                                                                             Sequence 17, Application US/10120018
Sequence 17, Application US/10120018
Publication No. US20030194708A1
GENERAL INFORMATION:
APPLICANT: Binnerts et al
TITLE OF INVENTION: Human Homolog of Crossveinless Materials and Methods
TILE REFERENCE: 28110/37995
CURRENT APPLICATION NUMBER: US/10/120,018
CURRENT FILING DATE: 2002-04-10
NUMBER OF SEQ ID NOS: 17
SEQ ID NO 17
SEQ ID NO 17
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                                                                         h 83.3%; Score 35; DB 12; Length 462; Similarity 71.4%; Pred. No. 5.1e+02; 5; Conservative 2; Mismatches 0; Indels
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Pred. No. 5.1e+02;
2; Mismatches 0; Indels
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NAME/KEX: MISC FEATURE
LOCATION: (351)..(351)
OTHER INFORMATION: wherein "X" is unknown or other
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OTHER INFORMATION: wherein "X" is unknown or other
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NAME/KEY: MISC_FEATURE
             TYPE: PRT
CORGANISM: Mus musculus
US-10-016-248-58
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ORGANISM: Homo sapiens
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113 CVPVSSC 119
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Best Local Similarity
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Best Local Similarity
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LENGTH: 462
LENGTH: 462
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                                                                                             Length 464;
                                                                                         83.3%; Score 35; DB 14; Length 46
57.1%; Pred. No. 5.1e+02;
ive 3; Mismatches 0; Indels
                                                                                                                                                                                                                                                                          Sequence 4, Application US/10451417

Publication No. US20040110921A1

GENERAL INFORMATION:

APPLICANT: ORITA, Satoshi et al

TITLE OF INVENTION:

CURRENT APPLICATION NUMBER: US/10/451,417

CURRENT FILING DATE: 2003-06-23

PRIOR FILING DATE: 2000-12-28

NUMBER OF SEQ ID NOS: 5

SOFTWARE: Patentin Ver. 2.1

SEQ ID NO 4

LENTING DATE: 201
; NAME/KEY: MISC FEATURE
; LOCATION: (462)...(462)
; OTHER INFORMATION: wherein "X" is unknown or other
US-10-120-018-17
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                                                                          Query Match
Best Local Similarity 57.1.
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ORGANISM: Homo sapiens
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Matches 4, Conserva
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Sequence 29595, A
Sequence 27, Appl
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Sequence 29358, A
Sequence 2, Appli
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/cgm2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-09-252-991A-29358

US-08-718-388-7

US-08-718-388-9

US-08-38-106-11

US-09-38-105-11

US-09-39-105-11

US-09-39-105-12

US-09-252-991A-22994

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73.8	73.8	73.8	73.8	73.8	73.8	73.8	73.8	73.8	73.8	73.8	73.8	73.8	73.8	73.8	73.8	73.8	73.8
31	31	31	31	31	31	31	31	31	31	31	31	31	31	31	31	31	31
28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENT

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GENERAL INFORMATION:
APPLICANT: Lyun Doucette-Stamm et al
APPLICANT: Lyun Doucette-Stamm et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
TITLE OF INVENTION: ENTEROCOCCUS FAECALIS FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 032796-032
CURRENT APPLICATION NUMBER: US/09/134,000C
CURRENT FILING DATE: 1998-08-13
RIOR APPLICATION NUMBER: US 60/055,778
PRIOR FILING DATE: 1997-08-15
NUMBER OF SEQ ID NOS: 6812
SOFTWARE: Patentin version 3.1
SEQ ID NO 6380
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Pred. No. 83;
2; Mismatches
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83;
               Sequence 6380, Application US/09134000C
Patent No. 6617156
                                                                                                                                                                                                                                                                                                                                                          ORGANISM: Enterococcus faecalis
                                                                                                                                                                                                                                                                                                                                                                                                                        h 88.1%;
Similarity 71.4%;
5; Conservative
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507 CLPMTSC 513
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Matches 5; Conser
US-09-134-000C-6380
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                                                                                                                                                                                                                                                                                                                                         TYPE: PRT
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RESULT 2

US-09-252-991A-29358

US-09-252-991A-29358

Satent No. 6551795

GENERAL INFORMATION:

HELLONIT: Marc J. Rubenfield et al.

TITLE OF INVENTION:

REPERBENCE:

199-02-18

PRIOR PELLING DATE:

1999-02-18

PRIOR PELLING DATE:

1999-02-18

PRIOR PELLING DATE:

1998-02-18

PRIOR PELLING DATE:

1998-02-18

PRIOR PELLING DATE:

1998-07-27

WOMBER OF SEQ ID NOS:

33142

LENGTH:

1989-07-27

TYPE: PRT ORGANISM: Pseudomonas aeruginosa

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CORRESPONDENCE ADDRESS
                      ADDRESSEE: BIRCH, S
STREET: PO BOX 747
CITY: FALLS CHURCH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1183 CLPLASC 1189
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0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
APPLICANT: Hardy, Daniel M.
APPLICANT: Garbers, David L.
TITLE OF INVENTION: Species-Specific Egg-Binding Proteins of TITLE OF INVENTION: Sperm
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSE: Arnold, White & Durkee
STREET: P. O. Box 4433
CITY: Houston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            81.0%; Score 34; DB 2; Length 2476; 71.4%; Pred. No. 9.7e+02;
                                                                  81.0%; Score 34; DB 4; Length 394; 71.4%; Pred. No. 1.7e+02; ive 1; Mismatches 1; Indels
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| Patent No. 6271362
| GENERAL INFORMATION:
| APPLICANT: MORIKAWA, MINORU
| APPLICANT: HARADA, NAOKI
| TITLE OF INVENTION: GENE ENCODING IGG FC REGION-BINDING
| TITLE OF INVENTION: PROTEIN
| NUMBER OF SEQUENCES: 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CITY:
STATE: Texa.
COMPTRY: USA
ZIP: 7710-4433
ZIP: 7710-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/276,967
FILING DATE: Submitted Herewith
CLASSIFICATION: 530
ATTORNEY/AGRNT INFORMATION:
NAME: Kitchell, Barbara S.
REFERENCE/DOCKET NUMBER: UTSD:418\KIT
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECHORS.
79-0924
TRUERAX: 713-789-2679
TRUERAX: 713-789-2679
TRUERAX: 713-789-2679
TRUERAMENT TO INFORMATION:
TELECHORS.
THEREFORE TO INFORMATION:
TELECHORS.
THEREFOR TO INFORMATION:
THEREFOR TO INFORMATI
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Best Local Similarity 71.*.
                                                                          Query Match
Best Local Similarity 71.4
Matches 5; Conservative
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       US-09-252-991A-29358
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US-08-718-388-7
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US-08-276-967-2
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STREET: BO BOX 747

STREET: WALLS CHUNCH

COUNTIES: FALLS CHUNCH

COUNTIES: RALLS CHUNCH

COUNTIES: REAL CHUNCH

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GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                       81.0%; Score 34; DB 3; Length 5405; 71.4%; Pred. No. 2e+03; Live 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            78.6%; Score 33; DB 2; Length 280; 71.4%; Pred. No. 1.9e+02; tive 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STREET: 1155 Avenue of the Americas CITY: New York COUNTRY: USD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ZIP: 10036
COMPUTER READBLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/969,106
FILING DATE: 13.NOV-1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Misrock, S. Lealie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 7934-057
TELECHOME: 212-790-909
TELEFORMINICATION INFORMATION:
TELEFORMINICATION INFORMATION:
TELEFORMINICATION INFORMATION:
TELEFORMINICATION STOP-9990
TELEFORMI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Yang, M.
APPLICANT: Yang, M.
APPLICANT: Nandabalan, K.
APPLICANT: Schulz, V.
ITILE OF INVENTION: CDK2 INTERACTIONS
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 11, Application US/08969106
Patent No. 5986055
GENERAL INFORMATION:
                            SEQUENCE CHARACTERISTICS:
LENGTH: 5405 amino acids
TYPE: amino acid
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                         Conservative
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Best Local Similarity 71.4
Matches 5; Conservative
                                                                                                                                                             , MOLECULE TYPE: protein US-08-718-388-9
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; MOLECULE TYPE: protein
US-08-969-106-11
                                                                                                                                                                                                                                                                                                                                                                                                                                            |:|| ||
1183 CLPLASC 1189
                                                                                                                                                                                                                                    227 CVPATEC 233
                                                                                                                                            linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 CVPLTSC 7
                                                                                                                                 TOPOLOGY:
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Sequence 11, Application US/09338125 Patent No. 6521412

US-09-338-125-11

RESULT 7

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Gaps
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| Sequence 2, Application US/08875972
| Patent No. 5985564
| GENERAL INFORMATION:
| APPLICANT: HUNDINGTON POETER and Jinhue Li
| TITLE OF INVENTION: ASSAY FOR IDENTIFYING GENES
| TITLE OF INVENTION: CHROMOSOME NON-DISJUNCTION
| VUMBER OF SEQUENCES: 29
| CORRESPONDENCE ADDRESS:
| ADDRESSEE: HAMILTON, BROOK, SMITH & REYNOLDS, P.C. STREET: Two Militia Drive
| CITY: Lexington | STATE: Massachusetts
| COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         78.6%; Score 33; DB 4; Length 280; 71.4%; Pred. No. 1.9e+02; ive 0; Mismatches 2; Indels
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FOC COmpatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICANT: Yang, M.
APPLICANT: Nandabalan, K.
APPLICANT: Schulz, V.
TITLE OF INVENTION: CDK2 INTERACTIONS
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
STREED: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION:
PRIOR APPLICATION:
APPLICATION NUMBER: US/08/969,106
FILING DATE: 13-NOV-1997
ATTORNEY/AGENT INFORMATION:
NAME: Misrock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 7934-057
                                                                                                                                                                                                                                                                                                                                                                      OPERATING SYSTEM: DOS
SOFTWARE: FastESQ Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/338,125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELECOMMUNICATION INFORMATION TELEPHONE: 212-790-9090
                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM Compatible OPERATING SYSTEM: DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 280 amino acids
TYPE: amino acid
STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: 212-869-9741
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 71.4
Matches 5; Conservative
                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              unknown
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                                                                                                                                                                                                                      New York
: USA
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Sequence 29595, Application US/09252991A Patent No. 6551795
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 71.4%;
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 71.4%;
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     |:| |||
90 CMPPTSC 96
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-09-252-991A-33012
                                                                                                                                                                                                                                               ; ORGANISM: Pseudo
US-09-252-991A-22994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 12
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Pred. No. 2.4e+02;
1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   76.2%; Score 32; DB 4; Length 68; 83.3%; Pred. No. 72; 0; Indels ive 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 92, Application US/09904615; Patent No. 6566325; GAEKRAL INFORMATION:
APPLICANT: ROSEN et al.
TITLE REPERENCE: PZ032P1
CURRENT APPLICATION NUMBER: US/09/904,615; CIRRENT FILING DATE: 2001-07-16; PRIOR APPLICATION NUMBER: 09/511,554; PRIOR FILING DATE: 1998-08-25; PRIOR FILING DATE: 1998-08-31; NUMBER OF SEQ ID NOS: 170; SOFTWARE: PatentIn Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LOCATION: (68)
OTHER INFORMATION: Xaa equals stop translation
                FILING DATE: 08-AUG-97
CLASSIFCATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/002,448
FILING DATE: 16-AUG-1995
ATTONNEY/AGENT INFORMATION:
NAME: Granahan BSQ., Patricia
REGISTRATION NUMBER: 32,227
REFERENCE/DOCKET NUMBER: 4195-03PA
TELECOMUNICATION INFORMATION:
TELECOMUNICATION INFORMATION:
TELECOMUNICATION INFORMATION:
TELECOMUNICATION SEQ 1D NO: 2:
SEQUENCE CHARACTERISTICS:
LENGT: 376 anino acids
TYPE: anino acids
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 22994, Application US/09252991A
Patent No. 6551/955
GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
APPLICATION NUMBER: US/08/875,972
                                                                                                                                                                                                                                                                                                                                                                                                            78.6%;
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Matches 5, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 78.6
Best Local Similarity 71.4
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: protein US-08-875-972-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Homo sapiens
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US-09-252-991A-22994
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LOCATION: (68)
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Sequence 33012.

Sequence 33012.

Sequence 33012.

Sequence 33012.

Barent No. 6551795.

GENERAL INFORMATION:

APPLICANT: Marc J. Rubenfield et al.

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS;

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS;

TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

FILE REFERENCE: 107196.136

CURRENT PILING DATE: 1999-02-18

PRIOR PILING DATE: 1999-02-18

PRIOR PILING DATE: 1998-02-18

PRIOR PILING DATE: 1998-07-27

NUMBER: OF SEQ ID NOS: 33142

LENGTH: 150

LENGTH: 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
APPLICANT: Marc J. Rubenfield et al.
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS TITLE OF INVENTION: ARRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
CURRENT PAPLICATION NUMBER: US/09/252,991A
CURRENT PILING DATE: 1999-02-18
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 29595
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
TITLE REPERENCE: 107196.136
CURRENT APPLICATION NUMBER: US 60/074,788
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR APPLICATION NUMBER: US 60/074,190
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 22994
LENGTH: 142
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Pred. No. 1.5e+02;
1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 32; DB 4; Length 142;
Pred. No. 1.4e+02;
0; Mismatches 2; Indels
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us-09-761-636a-11.open.rai

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TYPE: amino acid
STRANDEDNESS: Unl
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INEW YORK
TRY: USA
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Best Local Similarity
Matches 5; Conserv
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296 IPLTSC 301
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US-08-231-565A-27
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH;
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STATE:
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THEIR USE IN DIAGNOSTIC AND THERAPEUTIC
METHODS
                                                                                     Score 32; DB 4; Length 382;
Pred. No. 3.6e+02;
0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 32; DB 2; Length 661;
Pred. No. 6.1e+02;
1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                     Sequence 27, Application US/08417174
Patent No. 5844075
GENERAL INFORMATION:
GENERAL INFORMATION:
TAPPLICANT: KAWAKAMI, YUTAKA, ROSENBERG,
TITLE OF INVENTION: MELANOMA ANTIGENS AND
TITLE OF INVENTION: METHODS
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORGAN & FINNEGAN, L.L.P.
STYRET: NEW YORK
STATE: NEW YORK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/417,174
FILING DATE: 05-ARR-1995
FILING DATE: 22-ARR-1994
CLASSIFICATION NUMBER: US/08/231,565
FILING DATE: 22-ARR-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: CAROL M GRUPPI
RECISTRATION NUMBER: 37,341
REFERENCE/DOCKET NUMBER: 2026-4124US
TELECOMMUNICATION INCORMATION:
THE PEDANNE: 7110, 150,4001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ZIP: 10154
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 14
US-08-417-174-121
; Sequence 121, Application US/08417174
; LENGTH: 382
; TYPE: PRT
: ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-29595
                                                                                     Query Match
Best Local Similarity 71.4%;
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEPHONE: (212) 758-4800
TELEFAX: (212) 751-6849
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 661
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRANDEDNESS: Unknown
TOPOLOGY: Unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5; Conservative
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296 IPLTSC 301
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Matches 5; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY:
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                                                                                   Query Match
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                                                                                          MELANOMA ANTIGENS AND
THEIR USE IN DIAGNOSTIC AND THERAPEUTIC
METHODS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 27, Application US/08231565A
Patent No. 5874560
GENERAL INFORMATION:
APPLICANT: KAWAKMI, YUTAKA; ROSENBERG,
APPLICANT: STEVEN A.
TITLE OF INVENTION: MELANOMA ANTIGENS AND
TITLE OF INVENTION: METHODS
NUMBER OF SEQUENCES: 43
CORRESPONDENCE ADDRESS:
ADDRESSE: MORGAN & PINNEGAN
STERET: 345 PARK AVENUE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 32; DB 2; Length 661;
Pred. No. 6.1e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Indels
GENERAL INFORMATION:

GENERAL INFORMATION:

APPLICANT: KAWAKAMI, YUTAKA; ROSENBERG,
APPLICANT: STEVEN A.

TITLE OF INVENTION: METANOMA ANTIGENS AND
TITLE OF INVENTION: THEIR USE IN DIAGNOST:
TITLE OF INVENTION: METHODS
NUMBER OF SEQUENCES: 126
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORGAN & FINNEGAN, L.L.P.
STREET: 345 PARK AVENUE
CITY: NEW YORK
STATE: NEW YORK
TOWNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/417,174
FILING DATE: 05-APR-1995
PRIOR APPLICATION NUMBER: US/08/231,565
FILING DATE: 22-APR-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
RAGISTRATION NUMBER: 37,341
REGISTRATION NUMBER: 37,341
REGISTRATION NUMBER: 37,341
                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELECOMMUNICATION INFORMATION
TELEPHONE: (212) 758-4800
TELEFAX: (212) 751-6849
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           76.2%;
83.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM: MEDIUM TYPE: FLOPPY DISK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEX: 421792
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5; Conservative
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COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/231,565A
FILING DATE: 22-APR-1994
CLASSIFICATION NUMBER: 37,341
REGISTRATION NUMBER: 37,341
RELECOMMUNICATION INFORMATION:
TELEFRANCE (212) 758-4800
FILES FAX: 42179
TELEFRANCE CARACTERISTICS:
LENGTH: 661
TYPE: amino acid
TYPE: mino acid
STRANDEDNESS: Unknown
COPOLOGY: Unknown
NOLOGY: Unkn
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GenCore version 5.1.6 (c) 1993 - 2004 Compugen Ltd. Copyright

OM protein - protein search, using sw model

5, 2004, 09:47:29; Search time 4.60606 Seconds (without alignments) 125.302 Million cell updates/sec September Run on:

US-09-761-636A-12 38 Title: Perfect score:

1 CVPLTC 6 Scoring table: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5

Searched:

283366 Total number of hits satisfying chosen parameters:

283366 seqs, 96191526 residues

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

PIR 78:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

SUMMARIES	A Q v	100.0 817	7 97.4 293 2 T27621 hymotherical pro-	5 92.1 1627 2 S65464 hrednandy-associa	4 89.5 367 2 T20914 hypothetical	3 86.8 332 2 I48933 adenosine recento	3 86.8 415 2 A54126 endothelin	0 transposase	3 86.8 637 2 T08050 probable eth	3 86.8 650 2 A34498 qlycoprot	3 86.8 1236 1 A53970	2 84.2 108 2 S12982	2 84.2 137 2 T26433 hypothetical	2 84.2 156 2 C81364 probable per:	2 84.2 252 2 B82659 two-compo	2 84.2 301 2 T40593 cvtoplasmic d	2 84.2 314 2 B43652	2 84.2 345 1 NBBO apolipoprotein H	2 84.2 398 2 A35281	2 84.2 425 2 T40610	2 84,2 518 2 AD1930	2 84.2 972 2 A30	2 84.2 1034 2 JC5598	2 84.2 4660 2 T42737	1 81.6 40 2 E45495 bera-defension-5 -	1 81.6 133 2 T29606	1 81.6 224 2 T27063 hypothetical	1 81.6 326 2 C69341 cohalt transm	1 81 6 414 2 TEODIO	+ 01:0 TT 7 TOOMTS
æ	Query Match L	100	9	92.1	89.5	86.8	86.8	86.8	86.8	86.8	86.8	84.2	84.2	84.2	84.2	84.2	84.2	84.2	84.2	84.2	84.2	84.2	84.2	84.2	81.6	81.6	81.6		81.6	
	Scor	38	37	35	34	33	33	33	33	33	33	32	32	32	32	32	32	32	32	32	32	32	32	32	31	31	31	31	31	
	Result No.		7	٣	4	Ŋ	9	7	œ	6	10	11	12	13	14	15		17	18	19	20	21	22	23	24	25	56	27	28	

mannose-1-phosphat hypothetical prote RES4-25 protein - probable salt-indu VLDL receptor prec hypothetical prote hypothetical prote P-glycoprotein - S rough deal protein hypothetical protein	Deta-defensin-7 - beta-defensin-9 - beta-defensin-3 - beta-defensin-6 - airway epithelial lingual antimicrob
AC3622 T24121 J50188 T01622 T04858 T26644 T29027 T130821 T13166 T13166	145495 145495 145495 747438 A56128
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471 588 718 822 862 1042 1313 1451 2098	1 4 4 4 6 6 5 5 6 7 7 4 4
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ALIGNMENTS

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		protein F08
7 770	674	othetical

norhabditis elegans

C;Species: Caenorhabditis elegans C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999 C;Accession: T25674

R;Le, T.; Waterston, R. submitted to the EMBL Data Library, December 1996 A;Description: The sequence of C. elegans cosmid F08D12. A;Reference number: Z20068

A;Accession: T25674
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DMA
A;Residues: 1-817 <LET>
A;Cross-references: EMBL:U80840; PIDN:AAB37929.1; GSPDB:GN00020; CESP:F08D12.6
A;Experimental source: strain Bristol N2; clone F08D12
C;Genetics:

A;Gene: CESP:F08D12.6 A;Map position: 2 A;Introns: 27/2; 329/3; 407/1; 477/3; 538/3; 622/2

Gaps ; 0 Query Match
Best Local Similarity 100.0%; Pred. No. 18;
Matches 6; Conservative 0; Mismatches 0; Indels

0

479 CVPLTC 484 1 CVPLTC 6 ò g

RESULT 2

hypothetical protein ZC504.5 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-0ct-1999 #sequence_revision 15-0ct-1999 #text_change 18-Feb-2000
C;Accession: T27621
R;Kershaw, J.
submitted to the EMBL Data Library, July 1995
A;Accession: T27621
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Accession: T27621
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Residues: 1-293 - WIL.>
A;Cross-references: EMBL:Z50029; PIDN:CAA90343.1; GSPDB:GN00028; CESP:ZC504.5

C; Genetics:

A;Gene: CESP:ZC504.5 A;Map position: X A;Introns: 40/3; 140/3; 173/3; 255/3

97.4%; Score 37; DB 2; Length 293; 83.3%; Pred. No. 12; Query Match Best Local Similarity ·.

Gaps

g ò

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C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 29-Sep-1999
C;Accession: 14993
R;Marquardt, D.L.; Walker, L.L.; Heinemann, S.
J. Immunol. 152, 4508-4515, 1994
A;Title: Cloning of Two Adenosine Receptor Subtypes From Mouse Bone Marrow-Derived Mast A;Title: Cloning of Two Adenosine Receptor PwID:8157966
A;Accession: 148933
A;Accession: 148933
A;Accession: mRNA
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Residues: 1-33 cRES
A;Cross-references: EMBL:U05673; NID:9498337; PIDN:AAA19001.1; PID:9498338
C;Superfamily: adenosine receptor Al
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C;Date: 07-Unl-1995 #sequence_revision 07-Unl-1995 #text_change 16-Uul-1999
C;Accession: A54126
R;Kumar, C.; Mwangi, V.; Nuthulaganti, P.; Wu, H.L.; Pullen, M.; Brun, K.; Aiyar, H.; M.; Biol. Chem. 269, 13414-13420, 1994
A;Title: Cloning and characterization of a novel endothelin receptor from Xenopus heart A;Reference number: A54126; MUID:94230448; PMID:817572
A;Accession: A54126
A;Accession: A
           A;Accession: T20914
A;Accession: T20914
A;Accession: T20914
A;Accession: DNA
A;Molecule type: DNA
A;Residues: 1-367 <WIL>
A;Cross-references: EMBL: 292782; PIDN: CAB07186.1; GSPDB: GN00023; CESP:F14F8.5
A;Experimental source: clone F14F8
C;Genetics:
A;Genetics:
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Pred. No. 50;
2; Mismatches
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Pred. No.
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A;Introns: 23/3; 97/2; 145/2; 301/2
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Best Local Similarity 66.7%;
Matches 4; Conservative
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83.3%;
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Best Local Similarity 83.3.
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A; Reference number: Z19346
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Best Local Similarity
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92 CIPVTC 97
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A; Residues: 77-1627 <KRS>

A; Residues: 77-1627 <KRS>

A; Cross-references: GB:X62280; NID:G394649; PIDN:CAA48341.1; PID:G384650

B; Oxvig, C.; Sand, O.; Kristensen, T.; Gleich, G.J.; Sottrup-Jensen, L.

B; Disol. Chem. 268, 12243-12246, 1993

A; Title: Circulating human pregnancy-associated plasma protein-A is disulfide-bridged to

A; Reference number: 138097; MUID:93286045; PMID:7685339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A,Cross-references: EMBL:U28727
A;Note: the authors translated the codon CGA for residue 101 as Thr
R;Kristensen, T.; Oxvig. C.; Sand, O.; Moller, N.P.H.; Sottrup-Jensen, L.
Biochemistry 33, 1592-1598, 1994
A;Title: Amino acid sequence of human pregnancy-associated plasma protein-A derived from
A;Reference number: A54220; MUID:94146014; PMID:7508748
                                                                                                                                                                                                                                                                                                                                                                                             C;Species: Homo sapiens (man)
C;Date: 22-Nov-1996 #sequence revision 22-Nov-1996 #text_change 05-Nov-1999
C;Date: 22-Nov-1996 #sequence revision 22-Nov-1996 #text_change 05-Nov-1999
C;Accession: S65464; S65465; A54220; I38097
R;Haaning, J; Oxvig, C:; Overgaard, W.T.; Ebbesen, P.; Kristensen, T.; Sottrup-Jensen, submitted to the EMBL Data Library, June 1995
A;Accession: S65464
A;Accession: S65464
A;Accession: S65464
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A; Residues: 1-1627 < HRAA
A; Residues: 1-1627 < HRAA
A; Cross-references: EMBL: U28727; NID: g1142969; PIDN: AAC50543.1; PID: g1142970
A; Haaning, J.; Oxvig, C.; Overgaard, M.T.; Ebbesen, P.; Kristensen, T.; Sottrup-Jensen,
Bur. J. Biochem. 237, 159-163, 1996
A; Title: Complete cDNA sequence of the preproform of human pregnancy-associated plasma I
A; Reference number: S65463; MUID: 96203921; PMID: 8620868
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A;Map position: 9q33.1-9q33.1
F;1-22/Domain: signal sequence #status predicted <SIG>
F;23-80/Domain: propeptide #status predicted <PRO>
F;81-1627/Product: pregnancy-associated plasma protein A #status predicted <MAT>
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A;Residues: 77-1627 <RES>
A;Cross-references: EMBL:X68280; NID:g394649; PIDN:CAA48341.1; PID:g394650
C;Genetics:
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Pred. No. 1.1e+02;
1; Mismatches 0; Indels
       Indels
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           Mismatches
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Best Local Similarity 83.3%;
Matches 5; Conservative
               Conservative
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                                                                                                                                               123 CIPLTC 128
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A; Residues: 1-102 < HAW>
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83.3%;
Query Match
Best Local Similarity 83.3
Matches 5; Conservative
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A;Cross-references: GB:D29806
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Matches 5; Conserv
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A;Molecule type: mRNA
A;Residues: 1-108 <HER>
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T26433
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                                transposase all4675 [imported] - Nostoc sp. (strain PCC 7120)
CiSpecies: Nostoc sp. PCC 7120
A;Note: Nostoc sp. PCC 7120
A;Note: Nostoc sp. pcc 7120
A;Note: Nostoc sp. strain PCC 7120
C;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Dec-2002
C;Accession: AC3390
B;Kaneko, T.; Nakhamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Irriguchi Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S DNA Res. 8, 205-213, 2001
A;Aritle: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Ana A;Accession: AC3390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  probable ethylene receptor - muskmelon
C;Species: Cucumis melo (muskmelon)
C;Species: Cucumis melo (muskmelon)
C;Accession: T08050
R;Sato-Nara, K.; Yuhashi, K.; Higashi, K.; Hosoya, K.; Kubota, M.; Ezura, H.
submitted to the EMBL Data Library, December 1997
A;Description: Expression of an ERS homolog gene of melon (Cucumis melo L. reticulatus)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Glycoprotein antigen Bm86 precursor - southern cattle tick C;Species: Boophilus microplus (southern cattle tick)
C;Species: Boophilus microplus (southern cattle tick)
C;Date: 22-Jun-1990 #sequence_revision 22-Jun-1990 #text_change 21-Jul-2003
C;Accession: A34498
R;Rand, K.N.; Moore, T.; Sriskantha, A.; Spring, K.; Tellam, R.; Willadsen, P.; Cobon, A;Rand, K.N.; Moore, T.; Sriskantha, A.; Spring, K.; Tellam, R.; Willadsen, P.; Cobon, A;Title: Cloning and expression of a protective antigen from the cattle tick Boophilus A;Reference number: A34498; WUID:90099323; PMID:2690068
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A,Residues: 1-637 <SAT>
A,Cross-references: EMBL:AF037368; NID:g2707333; PIDN:AAC99477.1; PID:g2707334
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Pred. No. 94;
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Pred. No. 1.2e+02;
0; Mismatches 1; Indels
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C;Keywords: glycoprotein
F;209-246/Domain: EGF homology <EGF>
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83.3%;
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Best Local Similarity 83.3
Matches 5; Conservative
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Best Local Similarity 83.3
Matches 5; Conservative
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A;Molecule type: DNA
A;Residues: 1-467 <KUR>
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C, Superfamily: 1-phosphatidylinositol-4,5-bisphosphate phosphodiesterase II; 1-phosphati hodiesterase domain Y homology; SH2 homology; SH3 homology C, Keywords: phosphoric diester hydrolase
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C;Superfamily: dog hypothetical 12.2K protein (68K signal recognition particle region)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         F;336-468/Domain: 1-phosphatidylinositol-4,5-bisphosphate phosphodiesterase domain X F;889-688/Domain: SH2 homology <SH28-F;701-789/Domain: SH2 homology <SH28-F;701-789/Domain: SH2 homology <SH3>F;831-879/Domain: SH3 homology <SH3>
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  Length 650
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Pred. No. 1.2e+02;
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66.7%; Pred. No. 43;
cive 2; Mismatches
                                    0; Mismatches
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A;Cross-references: FlyBase:FBgn0003416
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Gaps

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Risimpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.; Briones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carrer, Fas-Neto, E.; Docena, C.; El-Dorry, H.; Facincani, A.P.; Ferreira, A.J.S. submitted to GenBank, June 2000
A;Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Frohm J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kurames, E.E.; Laigned, J.B.; Marchors: Martins, E.M.F.; Matsukuma, A.Y.; March, M.; Marca, E.C.; Miyaki, C.Y.; F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, M.C.; Mardins, E.M.; Marthors da Silva, A.C.R.; da Silva, F.R.; da Silva, A.C.R.; da Silva, A.C.R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C; Superfamily: response regulator with LytTR DNA-binding domain, AlgR/VirR/ComE type; r
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Pred. No. 86;
0; Mismatches 1; Indels
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Job time: 5.60606 secs
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Cipate: 31-Nar-2000 #equence_revision 31-Mar-2000 #text_change 03-Jun-2002
CiAccession: C81364
R;Parkhill, J; Wren, B.W.; Mungall, K.; Ketley, J.M.; Churcher, C.; Basham, D.; Chillin R;Parkhill, W.; Rajandream, M.A.; Rutherford, K.M.; VanVliet, A.; Whitehead, S.; Barrel Nature 403, 665-668, 2000
A;Title: The genome sequence of the food-borne pathogen Campylobacter jejuni reveals hyp. A;Reference number: A81250; MUD:20150912; PMID:10688204
A;Reference number: A81250; MUD:20150912; PMID:10688204
A;Reference preliminary
A;Molecule type: DNA
A;Residues: 1-156 <PAR>A;Residues: 1-156 <PAR>A;Residues: 0B:ALi39076; GB:ALi11168; NID:g6868128; PIDN:CAB73165.1; PID:g696834
A;Geneics: Cj6908
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C;Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 03-Jun-2002
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A.Residues: 1-252 <SIM>
A.Cross-references: GB.AE003989; GB.AE003849; NID:g9106666; PIDN:AAF84435.1; GSPDB:GN001
A.Experimental source: strain 9a5c
                                                                                                                                                                                                                                                                                                                                                                                                        A,Cross-references: EMBL:AL032631; PIDN:CAA21579.1; GSPDB:GN00019; CESP:Y106G6H.16
A,Experimental source: clone Y106G6H
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                     hypothetical protein Y106G6H.16 - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Date: 15-0ct-1999 #text_change 15-0ct-1999 (2,Accession: T26433 R;McMurray, A. submitted to the EMBL Data Library, October 1998 A;Reference number: Z20214 A;Reference number: Z20214
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A;Molecule type: DNA
A;Residues: 1-137 <WIL>
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A;Introns: 26/3; 61/3; 89/3
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A;Status: preliminary
A;Molecule type: DNA
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GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

September 5, 2004, 09:38:39; Search time 2.72727 Seconds (without alignments) 114.554 Million cell updates/sec Run on:

US-09-761-636A-12 38 1 CVPLTC 6 Title: Perfect score: Sequence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

141681 seqs, 52070155 residues Searched:

141681 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt_42:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description		500	rattı		homod	Synec	_		in				P50244 trypanosoma				P98164 homo sapien		•		homo	smint	_	٠.	Q92832 homo sapien	_	Q7z407 homo sapien	P46166 bos taurus	P46160 bos taurus	P46165 bos taurus	P46164 bos taurus	P46167 bos taurus	P46161 bos taurus
SUMMARIES	ID	CSM1 MOUSE		PDP2_RAT	PAPA_HUMAN	CSM2_HUMAN	TPIS_SYNEL	AA2B MOUSE			VANB_PSES9	APOH BOVIN	APOH_PANTR		MUB1 XENLA	CHRD_BRARE	LMG3 MOUSE	LRP2 HUMAN	LRP2_RAT	BD05 BOVIN	K121 HUMAN	K122_HUMAN	OB_SMICR	VOGO FOWPV	AVT_CATCO		- 1		- 1		- I	t	ŀ	BD03_BOVIN
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002775 bos taurus P2508 bos taurus P2508 bos taurus 075690 homo sapien P3434 caenorhabdi Q99117 homo sapien Q99104 mus musculu P26684 rattus norv P21450 bos taurus P25101 homo sapien Q61614 mus musculu Q29010 sus scrofa
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ALIGNMENTS

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RESULT 2
CSM1 HUMAN STANDARD; PRT; 3565 AA.

ID CSM2 (2001); Q96RM4;

AC Q96RZ7; Q96QU9; Q96RM4;

DT 15-MAR-2004 (Rel. 43, Last sequence update)

DT 15-MAR-2004 (Rel. 43, Last sequence update)

DT 15-MAR-2004 (Rel. 43, Last annotation update)

DT 15-MAR-2004 (Rel. 43, Last annotation update)

DT CUB and sushi multiple domains protein 1 precursor (UNQ5952/PRO19863).

GN CSMD1 OR KIAA1890.
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Best Local Similarity 83.3%;
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CUB AND SUSHI MULTIPLE DOMAINS PROTEIN 1.
EXTRACELLULAR (POTENTIAL).
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CYTOPLASMIC (POTENTIAL)
                                                                                                                                                     Isold=Q923L3-3; Sequence=VSP_009036;
Note=No experimental confirmation available;
-!- SIMILARITY: Belongs to the CSMD family.
-!- SIMILARITY: Contains 14 CVB domains.
-!- SIMILARITY: Contains 28 Sushi (SCR) domains.
                                                                              Name=2;
IsoId=Q923L3-2; Sequence=VSP_009037;
Note=No experimental confirmation available;
                       Event=Alternative splicing; Named isoforms=3;
                                                              IsoId=Q923L3-1; Sequence=Displayed;
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CUB 9.
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EMBL; AK038679; BAC30095.1; ALT_INIT.
EMBL; AK082377; BAC38482.1; -.
MGD; MGI:2137383; Csmdl.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR000859; CUB.
InterPro; IPR000436; Sushi_SCR_CCP.
Pfam; PR001431; CUB; 14.
Pfam; PR001084; sushi; 28.
SWART; SM00032; CCP; 28.
SWART; SM00042; CUB; 14.
PROSITE; PS01180; CUB; 14.
Repeat; Signal; Transmembrane; Sushi; Repeat; Signal; Repeat; Signal; Transmembrane; Sushi; Repeat; Signal; Transmembrane; Signal; Transmembrane; Signal; Transmembrane; Sushi; Repeat; Signal; Transmembrane; Signal; 
         ALTERNATIVE PRODUCTS:
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Kawakami B., Sugiyama A., Takemoto M., Sugiyama T., Irie R., Otsuki T., Sato H., Ota T., Wakamatsu A., Ishii S., Yamamoto J., Isono Y., Kawai-Hio Y., Saito K., Nishikawa T., Kimura K., Yamashita H., Matsuo K., Nakamura Y., Sekine M., Kikuchi H., Kanda K., Wagatua M., Murakawa K., Kanehori K., Takahashi-Fujii A., Oshima A., Suzuki Y., Sugano S., Nagahari K., Masuho Y., Nagai K., Isogai T.; Submitted (JUL-2003) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TISSUE=Brain,
MEDLINE=21456161; PubMed=11572484;
Nagase T., Kikuno R., Ohara O.;
Nagase T., Kikuno R., Ohara O.;
Prediction of the coding sequences of unidentified human genes. XXI.
The complete sequences of 60 new cDNA clones from brain which code for
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE-22887296; PubMed=12975309;
Clark H.P., durney A.L., Abaya E., Baker K., Baldwin D., Brush J.,
Clark H.P., durney A.L., Abaya E., Baker K., Baldwin D., Brush J.,
Chen J., Chow B., Chui C., Crowley C., Currell B., Deuel B., Dowd P.,
Baton D., Foster J., Grimaddi C., Gu Q., Hass P.E., Heldens S.,
Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J.,
Lewis L., Liao D., Mark M., Robbie E., Sanchez C., Schoenfeld J.,
Seshagiri S., Simmons L., Singh J., Smith V., Schinson J., Vagts A.,
Vandlen R., Watanabe C., Wieand D., Woods K., Xie M.-H., Yansura D.,
Xi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A., Wood W.I.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "The secreted protein discovery initiative (SPDI), a large-scale effort to identify novel human secreted and transmembrane proteins:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE OF 966-2013 FROM N.A. (ISOFORM 4), AND TISSUE SPECIFICITY
  Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                 SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
MEDLINE=21365705; PubMed=11472063;
Sun P.C., Uppaluri R., Schmidt A.P., Pashia M.E., Quant E.C.,
Sunwoo J.B., Gollin S.M., Scholnick S.B.;
"Transcript map of the 8p23 putative tumor suppressor region.";
Genomics 75:17-25(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -- FUNCTION: Potential suppressor of squamous cell carcinomas.
-- SUBCELLULAR LOCATION: Type I membrane protein (Potential).
-- ALTERNATIVE PRODUCTS:
Event=Alternative splicing; Named isoforms=4;
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IsoId=096P27-2; Sequence=VSP_009034, VSP_009035;
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Scholnick S.B., Richter T.M.;
"The role of CSMD1 in head and neck carcinogenesis.";
Genes Chromosomes Cancer 38:281-283(2003).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Genome Res. 13:2265-2270(2003).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           large proteins.";
DNA Res. 8:179-187(2001).
                                            NCBI TaxID=9606;
                                                                                                                                                                                                                                                         TISSUE=Brain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Godowski P.;
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                -I-TISSUE SPECIFICITY: Weakly expressed in most tissues, except in brain. Expressed at intermediate level in brain, including cerebellum, substentia nigra, hippocampus and feral brain.
-I-DISEASE: Defects in CSMD1 may be a cause of oral and oropharyngeal squamous cell carcinomas (OSCCS). Ref.5 and Ref.6 are however in disagreement: while Ref.6 considers CSMD1 as a strong candidate for OSCCS, Ref.5 thinks it is not.
-I-SIMILARITY: Belongs to the CSMD family.
-I-SIMILARITY: Contains 14 CUB domains.
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         IsoId=096PZ7-4; Sequence=VSP_009032, VSP_009033;
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InterPro; IPR000859; CUB.
InterPro; IPR000436; Sushi, SCR_CCP.
Pfam; PF000431; CUB; 14.
Pfam; PF00084; sushi, 27.
SWART; SM00042; CUB; 14.
PROSITE; PS01180; CUB; 14.
REPEAT; SYGNA1180; CUB; 14.
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EMBL, AK126936; BAC86754.1; ALT INIT.
EMBL, AY358174; AAQ88541.1; ALT INIT.
EMBL, AB067477; BAB67783.1; -.
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
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precursor (EC 3.1.3.43) (PDP 2) (Pyruvate dehydrogenase phosphatase,
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PDP2_RAT
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MEDLINE=98316337; PubMed=9651365;

Huang B., Gudi R., Wu P., Harris R.A., Hamilton J., Popov K.M.;

Huang B., Gudi R., Wu P., Harris R.A., Hamilton J., Popov K.M.;

Huang B., Gudi R., Wu P., Harris R.A., Hamilton J., Popov K.M.;

Huang B., Gudi R., Wu P., Harris R.A., Hamilton J., Popov K.M.;

To caid sequences, expression, and regulation.";

Biol. Chem. 273:17680-17688(1998).

Treactivation of the alpha subunit of the El component of the alpha subunit of the El component of the pyruvate dehydrogenase complex.

Treactivation of the alpha subunit of the El component of the pyruvate dehydrogenase (lipoamide)] + phosphate.

THINTION: CATALYTIC ACTIVITY: [Pyruvate dehydrogenase (lipoamide)] + phosphate.

THINTICH ACTIVITY: Heterodimer of a catalytic subunit and a FAD protein of unknown function (By similarity).

SUBUNIT: Heterodimer of a catalytic subunit and a FAD protein of unknown function (By similarity).

SUBCELLULAR LOCATION: Mitochondrial matrix.

TISSUE SPECIFICITY: Highly expressed in liver.

TISSUE SPECIFICITY: Highly expressed in liver.
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TISSUE=Placenta;

MEDLINE=96203921; PubMed=8620868;

Haaning J., Oxvig C., Overgaard M.T., Ebbesen P., Kristensen T.,

Sottrup-Jensen L.;

"Complete CDNA sequence of the preproform of human pregnancy-
associated plasma precein-A. Bvidence for expression in the brain and
induction by CAMP.":
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TRANSIT 68 530 [PYRUVATE DEHYDROGENASE [LIPOAMIDE]]-
FRAIN 68 530 [PYRUVATE DEHYDROGENASE [LIPOAMIDE]]-
SEQUENCE 530 AA; 59654 MW; 5AB688FAC78AD9CD CRC64;
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
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Pred. No. 9.8;
1; Mismatches 0; Indels
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InterPro; IPR001932; PP2C-like.
InterPro; IPR000222; PP2C.
Ffam; PF00481; PP2C; 2
SMART; SM00331; PP2C SIG; 1.
SMART; SM00332; PP2CC; 1.
PROSITE; PS01032; PP2C; 1.
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"Expression of recombinant human pregnancy-associated plasma protein-A and identification of the proform of eosinophil major basic protein as its physiological inhibitor.";
J. Biol. Chem. 275:31128-31133(2000).
                                                                                                                                                                                                                                                                                                                                          Oxvig C., Sand O., Kristensen T., Gleich G.J., Sottrup-Jensen L.,
"Circulating human pregnancy-associated plasma protein-A is disulfide-
bridged to the proform of eosinophil major basic protein.";
J. Biol. Chem. 268:12243-12246(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE-95057018; PubMed=7526035; Bonno M., Oxvig C., Kephart G.M., Wagner J.M., Kristensen T., Sottrup-Jensen L., Gleich G.J.;
"Localization of pregnancy-associated plasma protein-A and colocalization of pregnancy-associated plasma protein-A messenger ribonucleic acid and eosinophil granule major basic protein messenger ribonucleic acid in placenta."; Invest. 71:560-566(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Lawrence J.B., Oxvig C., Overgaard M.T., Sottrup-Jensen L., Gleich G.J., Hays L.G., Yates J.R. III, Conover C.A., "The insulin-like growth factor (IGF)-dependent IGF binding protein-4 protease secreted by human fibroblasts is pregnancy-associated plasma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Vergaard M.T., Sorensen E.S., Stachowiak D., Boldt H.B.,
Kristensen L., Sortrup-Jensen L., Oxvig C.;
"Complex of pregnancy-associated plasma protein-A and the proform of
eosinophil major basic protein. Disulfide structure and carbohydrate
J. Biol. Chem. 278:2106-2117(2003).
[2] SEQUENCE OF 77-1627 FROM N.A., SEQUENCE OF 81-98; 117-126; 210-224; 466-485; 507-519; 576-593; 609-621; 718-736; 742-754; 1006-1017; 1259-1273; 1369-1374; 1398-1398; 1490-1509; 1524-1533 AND 1537-1544, VARIANT SER-944, AND TISSUE SPECIFICITY.
                                                                                                                                          Kristensen T., Oxvig C., Sand O., Moller N.P.H., Sottrup-Jensen L., "Amino acid sequence of human pregnancy-associated plasma protein-A derived from cloned cDNA.

Biochemistry 33:1592-1598(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                             PARTIAL SEQUENCE, CARBOHYDRATE-LINKAGE SITES, AND DISULFIDE BONDS MEDLINE=22421368; PubMed=12421832;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TISSUE SPECIFICITY, AND DEVELOPMENTAL STAGE.

MEDLINE=99423540; PubMed=10491647;
Overgaard M.T., Oxvig C., Christiansen M., Lawrence J.B.,
Conover C.A., Glaich G.J., Sottrup-Jensen L., Haaning J.;
"Messenger ribonucleic acid levels of pregnancy-associated plasma protein—A and the profform of eosinophil major basic protein:
expression in human reproductive and nonreproductive tissues.";
Biol. Reprod. 61:1083-1089(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=20469470; PubMed=10913121;
Overgaard M.T., Haaning J., Boldt H.B., Olsen I.M., Laursen L.S.,
Christiansen M., Gleich G.J., Sottrup-Jensen L., Conover C.A.,
                                                                                                                                                                                                                                                               718-736; 742-754; 1259-1273; 1369-1374; 1490-1509; 1524-1533 AND 1537-1544, SUBUNITS, AND INTERCHAIN DISULFIDE BOND.
                                                                                                                                                                                                                                        SEQUENCE OF 81-89; 117-126; 210-224; 460-485; 507-519; 576-593;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IDENTIFICATION, FUNCTION, SUBCELLULAR LOCATION, AND TISSUE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Proc. Natl. Acad. Sci. U.S.A. 96:3149-3153(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FUNCTION, SUBUNITS, AND ENZYME REGULATION.
                                                                                                                                                                                                                                                                                                                      MEDLINE=93286045; PubMed=7685339;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=99179030; PubMed=10077652;
                                                                                                                       MEDLINE=94146014; PubMed=7508748;
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DEVELOPMENTAL STAGE.
MEDLINE=95293954; PubMed=7539791;
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                                                                                                                                                                                                                          of PRG2.

-1- SUBGNIT: Homodimer; disulfide-linked In pregnancy serum, predominantly found as a disulfide-linked 2:2 heterotetramer with the proform of PRG2.
-1- SUBCELDUAR LOCATION: Secreted.
-1- TISSUE SPECIFICITY: High levels in placenta and pregnancy serum. In placenta, expressed in X cells in septa and anchoring villi, and in syncytiotrophoblasts in the chorionic villi. Lower levels are found in a variety of other tissues including kidney.
-1- Good, fibroblasts and osteoblasts.
-1- DEVELOPMENTAL STAGE: Present in serum and placenta during pregnancy; levels increase throughout pregnancy.
-1- INDUCTION: By * B-bromoadenosine-3', 5'-phosphate.
-1- INDUCTION: By * B-bromoadenosine-3', 5'-phosphate.
-1- INDUCTION: By * B-bromoadenosine-3', 5'-phosphate.
-1- FPM: There appear to be no free sulfhydryl groups.
-1- SIMILARITY: Belongs to peptidase family M43B.
Oxvig C., Haaning J., Kristensen L., Wagner J.M., Rubin I., Stigbrand T., Gleich G.J., Sottrup-Jensen L.;
"Identification of angiotensinogen and complement C3dg as novel proteins binding the proform of eosinophil major basic protein in human pregnancy serum and plasma.";
J. Baol. Chem. 270:13645-13651(1995).
-! FUNCTION: Metalloproteinase which specifically cleaves IGFBP-4 in the presence of IGF, resulting in release of bound IGF.
-!- CATALYTIC ACTIVITY: Cleavage of the 135-Met-|-Lys-136 bond in insulin-like growth factor binding protein (IGFBP)-4, and the 143-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hydrolase; Metalloprotease; Metal-binding; Zinc; Signal; Glycoprotein;
Zymogen; Repeat; Sushi.
                                                                                                                                                                           Ser-|-Lys-144 bond in IGFBP-5.
COFACTOR: Binds 1 zinc ion per subunit (By similarity).
ENZYME REGULATION: Inhibited by complexation with the proform
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GO; GO: 0008237; F:metallopeptidase activity; IDA.
GO; GO:0008237; F:metallopeptidase activity; IDA.
GO; GO:0008237; F:metallopeptidase activity; IDA.
GO; GO:0008237; F:metallopeptidase activity; IDA.
GO; GO:0007565; P:pregnancy; NAS.
InterPro; IPR00895; Cond like_lec_gl.
InterPro; IPR00805; Land like_lec_gl.
InterPro; IPR008056; Land like_lec_gl.
InterPro; IPR008055; Pept M Zn BS.
InterPro; IPR008056; Sushi, SCR_CCP.
Ffam; PF00804; Sushi, 4.
SMART; SM00306; LandGL; 1.
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ARG-RICH.
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PROSITE; PS00142; ZINC_PROTEASE; 1.
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EMBL; X68280; CAA48341.1; -.
PIR; S65464; S65464.
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Genew; HGNC:8602; PAPPA.
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272
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the EMBL/GenBank/DDBJ databases.

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Submitted (JUL-2003)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Name=1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                       PRG2 PROFORM)
                                                                                                                                                                                                                          INTERCHAIN (WITH C-51 IN PRG2 PROFORM)
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CSM2 HUMAN STANDARD; PRT; 3487 AA.

GYZ406 QR056, Q9H4W0; Q9H4W1; Q9H4W1; Q9H4W1; Q9H4W3; Q9H4W3; Q9H4W3; Q9H4W3; Q9H4W3; Q9H4W3; Q9HCY5; Q9HCY7; Q9HCY8; Wan. Created)

15-MAR-2004 (Rel. 43, Last amnotation update)

CUB and sushi multiple domains protein 2.
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              (BY SIMILARITY)
                                                             (BY SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 35; DB 1; Length 1627; Pred. No. 30;
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                                                                                                                                                                                                                                                                                                                                                                       INTERCHAIN (WITH C-169 IN
              ZINC (CATALYTIC)
BY SIMILARITY.
ZINC (CATALYTIC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1; Mismatches
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OR 587-600.
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Similarity 83.3%;
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
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                                                                                                                                                                                                                                                                                  MEDINREZISUREZY, Pubmed 1.44/942.

A Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Schuler G.D., Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D., Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Stapleton M., Soares M.B., Bonaldo M.F., Casavan T.L., Schetz T.E., Stapleton M.J. Usdin T.B., Tonshiyuki S., Carninci P., Prange C., A. Brownstein M.J. Usdin T.B., Tonshiyuki S., Carninci P., Prange C., A. Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunzarane P.H., Richards S., Worley K.C., Hals S., Garcia A.M., Gay L.J., Hulyk S.W., Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Halton E., Ketteman M., Madan A., Rodrigues S., Sanchez A., Mitting M., Madan A., Young A.C., Sheychenko Y., Bouffard G.G., Mutting M., Madan A., Young A.C., Sheychenko Y., Bouffard G.G., Blakealey R.W., Touchman J.W., Green E.D., Dickson M.C., Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E., Beneration and initial analysis of more than 15,000 full-length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Note=No experimental confirmation available;
-!- TISSUE SPECIFICITY: Weakly expressed in most tissues, except in brain. Expressed at intermediate level in Drain, including cerebellum, substantia nigra, hippocampus and fetal brain. Overexpressed in some head and neck cancer cell lines.
-!- SIMILARITY: Belongs to the CSMD family.
-!- SIMILARITY: Contains 14 CUB domains.
-!- CAUTION: Ref.3 sequence differs from that shown due to a frameshift in position 939 that shortens the protein by 1021 residues in its N-terminus. It is unknown whether the sequence shown exists or whether Ref.3 is right, shortening the sequence in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nagase T., Kikuno R., Ohara O., "Prediction of the coding sequences of unidentified human genes. XXI. The complete sequences of 60 new cDNA clones from brain which code for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  sequence differs from that shown due to erroneous
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                                                                     to the EMBL/GenBank/DDBJ databases.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              human and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
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Name=2;
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                                                                                                                                                                                                                                                               MEDLINE=22388257; PubMed=12477932;
                                                                                                                                                                       SEQUENCE FROM N.A. (ISOFORM 3).
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DNA Res. 8:179-187(2001).
-!- ALTERNATIVE PRODUCTS:
                                     Wallis J., Brown A.;
submitted (SEP-2000)
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SEQUENCE FROM N.A.
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us-09-761-636a-12.open.rsp

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TPIS SYNEL
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R HSSP; P109308; 1VVD.

R Chnew; HGNC:19290, CSMD2.

R InterPro; IPR000859; CUB.

NR InterPro; IPR000436; Sushi_SCR_CCP.

DR Pfam; PF00084; Sushi; 26.

DR SMART; SM00032; CCP; 26.

DR SMART; SM00042; CUB; 14.

DR REPEA; TAINSMEMDIANCE; SUShi; Alternative splicing.

NW REPEA; TAINSMEMDIANCE; Sushi; Alternative splicing.

NWATH REPEA; TAINSMEMDIANCE; SUSHI; Alternative splicing.
                   AC112285; "NOT ANNOTATED CDS.
AC112286; "NOT ANNOTATED CDS.
AC1121890; CACC5319.1; ALT SEQ.
AL121990; CACC5319.1; ALT SEQ.
AL121990; CACC5321.1; ALT SEQ.
AL351990; CACC5321.1; ALT SEQ.
AL355178; CAC10283.1; ALT SEQ.
AL355178; CAC10284.1; ALT SEQ.
AL355178; CAC10286.1; ALT SEQ.
AL355178; CAC10286.1; ALT SEQ.
AL355178; CAC10286.1; ALT SEQ.
AL355178; CAC10286.1; ALT SEQ.
AL355178; CAC10289.1; ALT SEQ.
AL355178; CAC10289.1; ALT SEQ.
AL355178; CAC10289.1; ALT SEQ.
AL355178; CAC10290.1; ALT SEQ.
AL567106; "NOT ANNOTATED CDS.
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      BAC04593.1; ALT_INIT
BAC87101.1; -.
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AK127722;
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-!- PATHWAY: Plays an important role in several metabolic pathways.
-!- SUBUNIT: Homodimer (By similarity).
-!- SIMILARITY: Belongs to the triosephosphate isomerase family.
                                                    (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN=BP-1;
STRAIN=BP-1;
MEDLINE=2225144; PubMed=12240834;
Nakamura Y., Karoh H., Sasamoto Nakamura Y., Kishida Y.,
Natanaba A., Iriguchi M., Kawashima K., Kimura T., Kishida Y.,
Kiyokawa C., Kohara M., Matsumoto M., Matsuno A., Nakazaki N.,
Shimpo S., Sugimoto M., Takeuchi C., Yamada M., Tabata S.,
"Complete genome structure of the thermophilic cyanobacterium
Thermosynechococcus elongatus BP-1."
DNA Res: 91123-130(2002)
                                                                                                                                                                                                                                                                                                                      (POTENTIAL) .
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Pred. No. 63;
1; Mismatches 0; Indels
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15-MAR-2004 (Rel. 43, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
15-MAR-2004 (Rel. 43, Last annotation update)
Triosephosphate isomerase (EC 5.3.1.1) (TIM).
TPIA OR TPI OR TLR0966.
Synechococcus elongatus (Thermosynechococcus elongatus).
Bacteria, Cyanobacteria, Chroococcales; Synechococcus.
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HAMAP; MF_00147; -; 1.
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ilarity 83.3%;
Conservative
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     Query Match
Best Local Similarity
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2588 CVPVTC 2593
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EXTRACELLULAR (POTENTIAL)

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NCBI_TaxID=6941;
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ID BM86 BOOMI
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CARBOHYD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Margardt D.L., Walker L.L., Heinemann S.;
"Cloning of two adenosine receptor subtypes from mouse bone marrow-derived mast cells.", IS2:4508-4515 (1994).
-: FUNCTION: Receptor for adenosine. The activity of this receptor is mediated by G proteins which activate adenylyl cyclase.
-: SUBCELLULAR LOCATION: Integral membrane protein.
-: SUBCELLULAR Belongs to family 1 of G-protein coupled receptors.
                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                  Pfam; PF00121; TIM; 1.
ProDom; PD001005; Triophos ismrse; 1.
TIGREAMS; TIGRE00419; Lim; 1.
PROSITE; PS00171; TIM; 1.
PROSITE; PS00171; TIM; 1.
PROSITE; PS00171; TIM; 1.
PROSITE; PS00171; TIM; 1.
ACT_SITE II8 II8 BY SIMILARITY.
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                                                                                                                                                                                                               Length 265;
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PROSITE; PS00262; G PROTEIN RECEP_F1_2; 1.
G-protein coupled receptor; Transmembrane; Glycoprotein; Lipoprotein; Palmitate.

EXTRACELLULAR (POTENTIAL).

PRANSINE 1 (POTENTIAL).

DOMAIN 32 44 CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                      1; Indels
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3 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
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BY SIMILARITY.
; 92A0D6015B51927A CRC64;
                                                                                                                                                                                                               86.8%; Score 33; DB 1;
83.3%; Pred. No. 12;
tive 0; Mismatches 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
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    InterPro; IPR000652; Triophos_ismrse.
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InterPro; IPR000276; GPCR Rhodpsn.
Pfam; PF00001; 7tm 1; 1.
PRINTS; PR00237; GPCRRHODOPSN.
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MEDLINE-94209670; PubMed-8157966;
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187 187 BY
265 AA; 29096 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; U05673; AAA19001.1; -. PIR; 148933. HSSP; P29274; IMMH.
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Matches 5; Conservative
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Q60614;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TISSUE=Gut;
MEDLINE=90099323; PubMed=2690068;
Rand K.N., Moore T., Sriskantha A., Spring K., Tellam R.L.,
Willadsen P., Cobon G.S.;
"Cloning and expression of a protective antigen from the cattle tick
Boophilus microplus.";
                                                                                                                                                                                                                                                                                                                                                                               Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Willadsen P., Riding G.A., McKenna R.V., Kemp D.H., Tellam R.L., Nielsen J.N., Lahnstein J., Cobon G.S., Gough J.M.;
Nielsen J.N., Lahnstein J., Cobon G.S., Gough J.M.;
Immunologic control of a parasitic arthropod. Identification of a protective antigen from Boophilus microplus.";
J. Immunol. 143:1346-1351(1989).
-:- SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor
                                                                                                                                                                                           N-LINKED (GLCNAC. ..) (POTENTIAL).
N-LINKED (GLCNAC. ..) (POTENTIAL).
S-palmitoyl cysteine (Potential).
C843108371ADLCIC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-FEB-1991 (Rel. 17, Created)
01-FEB-1991 (Rel. 17, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
10-OCT-2003 (Rel. 42, Last annotation update)
Glycoprotein antigen BM86 precursor (Protective antigen).
Boophilus microplus (Cattle tick).
Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Acari;
Parasitiformes; Ixodida; Ixodidae; Boophilus.
                                                                                                                                                                                                                                                                                                                                                                                 ;
0
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                                                                                                EXTRACELLULAR (POTENTIAL)
                                             CYTOPLASMIC (POTENTIAL).
                                                                                                                     7 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Proc. Natl. Acad. Sci. U.S.A. 86:9657-9661(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           'FICDALIE'.
-!- SIMILARITY: Contains 7 EGF-like domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  650 AA
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                                                                  6 (POTENTIAL)
                     5 (POTENTIAL)
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                                                                                                                                                                                                                                                                                                                                                      Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PARTIAL SEQUENCE.
MEDLINE=89309823; PubMed=2745982;
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InterPro; IPR006209; BGF like.
InterPro; IPR065210; IBGF.
PFam; PF00008; EGF; 2.
SMART; SM00181; EGF; 2.
                                                                                                                                                                                                                                                                                 36064 MW;
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Best Local Similarity 85...
5; Conservative
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AA;
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3L J. Cell Biol. 145:605-618(1999).

1. FUNCTION: Binding to cells via a high affinity receptor, laminin of is thought to mediate the attachment, migration and organization of cells into tissues during embryonic development by interacting with other extracellular matrix components.

2. SUBUNIT: Laminim is a complex glycoprotein, consisting of three different polypeptide chains (alpha, beta, gamma), which are bound to each other by disulfide bonds into a cross-shaped molecule comprising one long and three short arms with globules at each end rising one long and three short arms with globules at each end some in second comprising one long and three short arms with globules at each comprising one long and three short arms with globules at each end arms a subcult. I subcation is a subunit of laminin-12.

2. SUBCELDUAR LOCATION: Extracellular.

2. SUBCELDUAR LOCATION: Extracellular.

3. SUBCELDUAR LOCATION: Dradly expressed in: skin, heart, lung, and the reproductive tracts.

3. SUBCELDUAR LOCATION: The alpha-helical domains I and II are thought to interact with other laminin chains to form a coiled coil structure.

3. SUMILARITY: Contains I laminin N-terminal domains.

3. SIMILARITY: Contains I laminin EGF-like domains.
                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Glycoprotein, Basement membrane; Extracellular matrix; Coiled coil;
Laminin EGF-like domain; Cell adhesion; Repeat; Signal.
SIGNAL 1 19 POTENTIAL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LAMININ GAMMA-3 CHAIN.
LAMININ GAMMA-3 CHAIN.
LAMININ BGF-LIKE 1.
LAMININ BGF-LIKE 2.
LAMININ BGF-LIKE 3.
LAMININ BGF-LIKE 4.
LAMININ BGF-LIKE 5.
LAMININ BGF-LIKE 6.
LAMININ BGF-LIKE 6.
LAMININ BGF-LIKE 7.
LAMININ BGF-LIKE 9.
LAMININ BGF-LIKE 10.
LAMININ BGF-LIKE 11.
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GO; GO:0005578; C:embrane; TAS.

GO; GO:000620; C:membrane; TAS.

GO; GO:000529; F:structural molecule activity; TAS.

InterPro; IPR006212; Lam N2.

InterPro; IPR00034; Laminin B.

InterPro; IPR00034; Laminin B.

InterPro; IPR0011; Laminin B.

InterPro; IPR00521; Laminin B.

IPR00521; Laminin B.

IPR00521; Laminin W.

IPR05371E; PS001186; EGF Li; T.

IPR05371E; PS001186; EGF Li; T.

IPR05371E; PS001186; EGF Li; T.

IPR05371E; PS01248; LAMININ TYPE EGF; 10.
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COLLED COIL (POTENTIAL).
COLLED COIL (POTENTIAL).
COLLED COIL (POTENTIAL).
COLLED COIL (POTENTIAL).
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MEDLINE=99242614; PubMed=10225960;
MEDLINE=99242614; Albus A., Jin W., Hunter D.D., Brunken W.J.,
Burgeson R.E., Champland M.F.;
"Characterization and expression of the laminin gamma3 chain: a novel,
non-basement membrane-associated, laminin chain.";
               GLYCOPROTEIN ANTIGEN BM86.
HYDROPHOBIC, REMOVED DURING MATURATION SIMILARITY).
EGF-LIKE 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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N-LINKED (GLCNAC. .) (POTENTIAL N-LINKED (GLCNAC. .) (POTENTIAL N-LINKED (GLCNAC. .) (POTENTIAL N-LINKED (GLCNAC. .) (POTENTIAL N-LINKED (GLCNAC. .) (POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 33; DB 1; Length 650;
Pred. No. 30;
0; Mismatches 1; Indels
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5DED71E354D8312A CRC64;
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15-MAR-2004 (Rel. 43, Last annotation update)
Laminin gamma-3 chain precursor (Laminin 12 gamma 3)
                                                                 EGF-LIKE 2.
EGF-LIKE 3.
EGF-LIKE 4.
EGF-LIKE 4.
EGF-LIKE 6.
EGF-LIKE 6.
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28-FEB-2003 (Rel. 41, Last seq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          71721 MW;
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182
348
382
235
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650 AA;
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SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 CVPLTC 6
                                                     NCBI_TaxID=9606;
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Q9Y6NG;
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LMG3_HUMAN
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263
268
271
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314 AA;
                                                                    Local Similarity
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                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                  J. Bacteriol. 170:4924-4930(1988).
-!- COFACTOR: FMN (By similarity).
-!- PATHWAY: Vanillate degradation (vanillate is a key intermediate in the degradation of lignin).
-!- SIMILARITY: Belongs to the PDR/vanB family.
-!- SIMILARITY: In the C-terminal section; belongs to the 2Fe2S plant-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pfam; PP00175; NAD binding 1; 1.
PRINTS; PR00409; PHDIOXRDTASE.
PR051TE; PS0191; PRESS PERESONIN; 1.
Aromatic hydrocarbons catabolism; Lignin degradation; Oxidoreductase; Flavoprotein; FMN; NAD; Metal-binding; Iron-sulfur; Iron; 2Fe-2S;
                                                                                                                                         Gaps
                                                                                                                                                                                                                                                   01-OCT-1989 (Rel. 12, Created)
01-OCT-1989 (Rel. 12, Last sequence update)
15-MAR-2004 (Rel. 43, Last amnotation update)
Vanillate O-demethylase oxidoreductase (EC 1.14.13.-) (Vanillate
                                                            (POTENTIAL) . (POTENTIAL) . (POTENTIAL) .
                                                                                                                                                                                                                                                                                                                                                                        Brunel F., Davison J.; "Cloning and sequencing of Pseudomonas genes encoding vanillate demethylase.";
                                          (POTENTIAL)
            (POTENTIAL) (POTENTIAL)
                                                                                                                                          .
                                 (POTENTIAL)
                                                                                         (POTENTIAL)
    ATTACHMENT SITE (POTENTIAL)
                                                                                                                      DB 1; Length 1587;
                                                                                                   MW; 3CB6E09B5F203319 CRC64;
                                                                                                                                         1; Indels
                                         (GLCNAC. . .)
(GLCNAC. . .)
(GLCNAC. . .)
                                                                                (GLCNAC. . .)
                                  (GLCNAC. . .)
                                                                       (GLCNAC. . .)
                                                                                            (GLCNAC
                                                                                                                                                                                                                                  314 AA
                                                                                                                                            Mismatches
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InterPro; IPR008333; FAD binding_6.
InterPro; IPR001041; Ferredoxin.
InterPro; IPR001433; Oxred_FAD/NAD(P).
InterPro; IPR000951; Phdiox reductase.
Pfam; PF00970; FAD binding_6; 1.
Pfam; PF00111; Fer2; 1.
                                                                                                                        Score 33;
Pred. No.
    CELL ATTAC
N-LINGED
                                                                                                                                                                                                                                                                                            degradation ferredoxin-like protein)
                                                                                                                                                                                                                                                                                                              Pseudomonas sp. (strain ATCC 19151).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FMN.
                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A. MEDLINE=89008117; PubMed=3170489;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; M22077; AAA26020.1; -.
HSSF; P33164; 2PIA.
                                                                                                                       86.8%;
                                                                                                     172051
                                                                                                                                                                                                                                                                                                                                                                                                                                                                type ferredoxin family.
                                                                                                                                                                                                                                                                                                                          Bacteria; Proteobacteria.
                                                                                                                                            5; Conservative
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                                                                                                                               Local Similarity
                                                                                                                                                               1 CVPLTC 6
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                       119
295
328
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P12580;
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NP BIND
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CARBOHYD
                                                              CARBOHYD
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                        CARBOHYD
                                   CARBOHYD
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Biochem. J. 267:261-264(1990)

- FONGTION: Binds to various kinds of negatively charged substances such as heparin, phospholipids, and dextran sulfate. May prevent activation of the intrinsic blood coagulation cascade by binding to phospholipids on the surface of damaged cells.

- GUBCELLUIAR LOCATION: Secreted.

- TISSUE SPECIFICITY: Expressed by the liver and secreted in plasma.
                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Amino acid sequence and location of the disulfide bonds in bovine beta 2 glycoprotein I: the presence of five Sushi domains."; Biochemistry 30:11687-11694(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE OF 4-345 FROM N.A., PARTIAL SEQUENCE, AND DISULFIDE BONDS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Bovinae; Bos.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      P17630; 028052;
01-AUG-1990 (Rel. 15, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Beta-2-glycoprotein I precursor (Apolipoprotein H) (Apo-H) (B2GPI)
(Beta(2)GPI).
(BY SIMILARITY).
(BY SIMILARITY).
(BY SIMILARITY).
(BY SIMILARITY).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gao B., Virmani M., Romm E., Lazar-Wesley E., Sakaguchi K.,
Appella E., Kunos G., Takacs L.,
Submitted (DEC-1992) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Complete primary structure of bovine beta 2-glycoprotein
                                                                                                                                                                                     Score 32; DB 1; Length 314;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bendixen E., Halkier T., Magnusson S., Sottrup-Jensen L.,
Kristensen T.;
                                                                                                                                                                                                                                                 1; Indels
                                                                                                                               FC521516AA6CEB72 CRC64;
      IRON-SULFUR (2FE-2S) (
IRON-SULFUR (2FE-2S) (
IRON-SULFUR (2FE-2S) (
IRON-SULFUR (2FE-2S) (
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                                                                                                                                                                                                                     Pred. No. 23;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         localization of the disulfide bridges.";
Biochemistry 31:3611-3617(1992).
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MEDLINE=90226328; PubMed=2327984;
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MEDLINE=92089075; PubMed=1751487;
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                                                                                                                               33706 MW;
                                                                                                                                                                                           84.2%;
                                                                                                                                                                                                                                                        4; Conservative
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            263
268
271
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bos taurus (Bovine).
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258 CIPLAC 263
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'Chimpanzee apolipoprotein H (beta2-glycoprotein I): report on the
                                                                                                                                                                                                                 Polymorphism.
SIGNAL
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  removed. Usage by and for commercial ant (See http://www.isb-sib.ch/announce/
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                                                                                                                                                                                                                                                                                                                        Gaps
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15-MAR-2004 (Rel. 43, Last annotation update)
Beta-2-glycoprotein I precursor (Apolipoprotein H) (Apo-H) (B2GPI)
(Beta(2)GPI).
                                                                                                                                                                                                                                                                                                                                                                                                                                 Pan troglodytes (Chimpanzee).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
                                                                                                                                                                                                                                                                                                                       ;
                                                                      Heparin-binding; Glycoprotein; Plasma; Repeat; Sushi; Signal.
SIGNAL 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                           [1] —
SEQUENCE FROM N.A., AND VARIANT GLU-229.
MEDLINE=21372074; PubMed=11479737;
Sanghera D.K., Nestlerode C.S., Ferrell R.E., Kamboh M.I.;
                                                                                                                                                                                                                                                                                                         DB 1; Length 345;
                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                            E117DAB609461C33 CRC64;
                                                                                    BETA-2-GLYCOPROTEIN I
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S (IN REF. 1).
N (IN REF. 1).
C (IN REF. 1).
C (IN REF. 1).
N (IN REF. 1).
N (IN REF. 1).
R (IN REF. 1).
R (IN REF. 1).
                                                                                                                                                                                                              (GLCNAC.
                                                                                                                                                                                                                           (GLCNAC.
                                                                                                                                                                                                                                                                                                                                                                                345 AA
                                                                                                                                                                                                                                                                                                       84.2%; Score 32; DB 66.7%; Pred. No. 26; ive 1; Mismatches
      entities requires a license agreement (S. or send an email to license@isb-sib.ch).
                                                                                                 SUSHI 2.
SUSHI 3.
SUSHI 4.
SUSHI-LIKE.
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N-LINKED
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N-LINKED
                        EMBL; L07303; AAA30382.1; -.
EMBL; X60065; CAA42669.1; -.
PIR; DN0502; NBBO.
HSSP; P02749; 1C1Z.
InterPro; IPR000436; Sushi_SCR_CCP.
Pfam; PF00084; sushi; 4.
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modified and this statement is not
                                                                                           SUSHI
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15-MAR-2004 (Rel. 43, Last sequ
15-MAR-2004 (Rel. 43, Last ann
                                                                                                                                                                                                                                                                                            38252 MW;
                                                                                                                                                                                                                                                                                                                     4; Conservative
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                                                                                  137 CAPITC 142
                                                                                                                                                                                                                                                                                                              Local Similarity
                                                                                                                                                                                                                                                                                                                                  1 CVPLTC 6
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0
gene Structure, a common polymorphism, and a high prevalence of antiphospholipid antibodies.";

Hum. Genet. 109:63-72/2001).

-!- FUNCTION: Binds to various kinds of negatively charged substances such as heparin, phospholipids, and dexrran sulfate. May prevent activation of the intrinsic blood coagulation cascade by binding to phospholipids on the surface of damaged cells.

-!- SUBCELLULAR LOCATION: Secreted (By similarity).

-!- TISSUE SPECIFICITY: Expressed by the liver and secreted in plasma.

-!- SIMILARITY: Contains 4 Sushi (SCR) domains.
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712A3EDA2AD4FD36 CRC64;
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BETA-2-GLYCOPROTEIN I.
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(Rel. 34, Last sequence update)
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SUSHI 2.
SUSHI 3.
SUSHI 4.
SUSHI -LIKE.
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Pred. No. 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL, AF358415, AAK71538.1;
EMBL, AF358408, AAK71538.1;
EMBL, AF358409, AAK71538.1;
EMBL, AF358410, AAK71538.1;
EMBL, AF358411, AAK71538.1;
EMBL, AF358411;
EMBL, AF358411;
EMBL, AF358411;
EMBL, AF358411;
EMBL, AF358413;
EMBL, AF358414;
EMRL, AF358414;
EM
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345 AA;
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Best Local Similarity
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DCAM TRYBB
ID DCAM TRYBB
AC P50244;
DT 01-0CT-1996 (;
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SO THE STATES THE STATES AND DRIVER OF SOCIOUS CONTRIBUTION OF SOCIOUS CONTRIB
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Spermidine biosynthesis; Lyase; Decarboxylase; Pyruvate; Zymogen, CHAIN 1 85 S-ADENOSYLMETHONINE DECARBOXYLASE BETA CHAIN (BY SIMILARITY).

CHAIN 86 370 S-ADENOSYLMETHIONINE DECARBOXYLASE ALPHA
                                                                                         Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma.
NCBL_TaxID=5702;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                    S-adenosylmethionine decarboxylase proenzyme (EC 4.1.1.50) (AdoMetDC) (SamDC) [Contains: S-adenosylmethionine decarboxylase alpha chain; S-adenosylmethionine decarboxylase beta chain].
Trypanosoma brucei brucei.
                                                                                                                                                                                                                                                                             Submitted (JAN-1995) to the EMBL/GenBank/DDBJ databases.
-!- CATALYTIC ACTIVITY: S-adenosyl-L-methionine = (5-deoxy-5-adenosyl) (3-aminopropyl) methylsulfonium salt + CO(2).
-!- COFACTOR: PYTUVOYJ group.
-!- PATHMAY: Decarboxylation of S-adenosylmethionine provides the aminopropyl moiety required for spermidine and spermine biosynthesis from putrescine.
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                                                                                                                                                                                    STRAIN=EATRO 164;
Scott J.R., Ullman B.;
"Molecular cloning and functional expression of the S-adenosylmethionine decarboxylase gene of Leishmania donovani and Trypanosoma brucei.";
Submitted (JAN-1995) to the EMBL/GenBank/DDBJ databases.
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                                                                                                                                                                                                                                                                                                                                                                                                                      SIMILARITY: Belongs to the eukaryotic AdoMetDC family.
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CLEAVAGE (NONHYDROLYTIC)
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01-0CT-1994 (Rel. 30, Last sequence update)
10-0CT-2003 (Rel. 42, Last annotation update)
10-0CT-2003 (Rel. 42, Last annotation update)
Nenopus laevis (African clawed frog).
      Last annotation update)
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Pfam; PF01536; SAM decarbox; 1.
ProtDom; PD002379; SAM decarbox; 1.
TICRFAMS; TICR00535; SAM DCame; 1.
PROSITE; PS01336; ADOMETDC; I.
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      16-OCT-2001 (Rel. 40,
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P38565,
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                                                                                                                                                                                                                                                                                                                                                                                            Voin milections described to the following the state of t
                                                                                                                                                                                            SECTENCE FROM N.A.
MEDLINE=91002513; PubMed=2207068;
Probet J.C., Gertzen B.-M., Hoffmann W.;
Printegumentary mucin (FIM-B.1) from Xenopus laevis homologous with
von Willebrand factor.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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1 (INCOMPILETO)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
Xenopodinae; Xenopus.
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Pred. No.
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InterPro; IPR006208; Cys knot.
InterPro; IPR006207; Cys knot.
InterPro; IPR001007; WWP_C.
Pfam; PP00007; Cys knot; 1.
SMART; SM00041; CT_ 1.
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                                                                                                                                  NCBI_TaxID=8355;
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PEQUENCE OF 1-42 FROM N.A.

Record of the control o
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                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
Cyprinidae; Danio.
                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A., FUNCTION, TISSUE SPECIFICITY, AND DEVELOPMENTAL
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CHRD 1.
CHRD 2.
CHRD 3.
CHRD 4.
VWFC 2.
VWFC 3.
VWFC 4.
N-LINKED (GLCNAC. . .) (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                      "Differential regulation of chordin expression domains in mutant
                                                                                                                                                                                                                                                                                                                                 TISSUE-Gastrula;
MEDLINE-98104254; PubMed=9441687;
Miller-Bertoglio V.E., Fisher S., Sanchez A., Mullins M.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Glycoprotein; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SIMILARITY: Belongs to the chordin family. SIMILARITY: Contains 4 CHRD domains. SIMILARITY: Contains 4 WWFC domains.
057472; Q9DEDB;
16-OCT--2001 (Rel. 40, Created)
16-OCT--2001 (Rel. 40, Last sequence update)
16-OCT--2003 (Rel. 42, Last annotation update)
Chordin precursor (Chordino protein).
                                                                                                                                            Brachydanio rerio (Zebrafish) (Danio rerio)
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CHORDIN.
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PROSITE; PS01208; VWFC 1; 3.
PROSITE; PS50184; VWFC 2; 4.
Developmental protein; Repeat;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL, AF034606, AAB93485.1; -.
EMBL, AB043968, BAB18642.1; -.
ZFIN; ZDB-GENE-990415-33; chd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Dev. Biol. 192:537-550(1997).
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InterPro; IPR001007; VWF_C.
Pfam; PF00093; VWc; 4.
SMART; SM00566; SOG; 3.
SMART; SM00214; VWC; 4.
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CARBOHYD
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SQ SEQUENCE 940 AA; 104999 MW; B8S5CAF84F4623AC CRC64;
Query Match
Best Local Similarity 83.3%; Pred. No. 69;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps
Qy 1 CVPLTC 6
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Db 815 CPPLTC 820

Search completed: September 5, 2004, 09:56:09 Job time : 3.72727 secs

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GenCore version 5.1.6 (c) 1993 - 2004 Compugen Ltd.
              Copyright
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OM protein - protein search, using sw model

September 5, 2004, 09:46:09; Search time 13.5758 Seconds (without alignments) 139.448 Million cell updates/sec Run on:

US-09-761-636A-12 38 Title: Perfect score:

1 CVPLTC 6 Sequence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

1017041 seqs, 315518202 residues Searched:

1017041 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Database

SPTREMBL 25:*
1: Sp archea:*
2: Sp_bacteria:*
3: Sp fungi:*
4: Sp_human:*
5: Sp_manmal:*
5: Sp_manmal:* unclassified: * vertebrate: * sp_rvirus:* sp_bacteriap:* sp_plant:*
sp_rodent:*
sp_virus:* 1010 1110 1121 1141 1151 1161 Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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SUMMARIES			ID		Q963E7	018280	07SKG4	09H4W4	0960119	09231.3	OBGRM4	FINIO	OPDGMZ	09JK57	OBOVW3	096003	098306	CRDAKE	DUL TOO	Q8K4K7	Q7Z408	O8H347	
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367	511	570	99	99	68	93	168	246	265	277	395	415	415	429	443	467	556	637		650	664	852	852	875	1007	1230	1230
89.5	89.5	89.5	86.8	86.8	86.8	86.8	86.8	86.8	86.8	86.8	86.8	86.8	86.8	86.8	86.8	86.8	86.8	86.8	86.8	86.8	86.8	86.8	86.8	86.8	86.8	86.8	86.8
3.4	34	34	33	33	33	33	33	33	33	33			33		33	33	33	33	33	33	33	33	33	33	33	33	33
17	19	20	21	22	23	24	25	26	27	28	29		31	32		34	35	36	37	38	99	40	41	42	43	44	45

ALIGNMENTS

Caenorhabditis elegans. Bukaryota, Metazoa, Nematoda, Chromadorea, Rhabditida, Rhabditoides, Rhabditidae, Peloderinae, Caenorhabditis. NCBI_TaxID=6239; Gaps ; Robertson H.M.;
"Gustatory related receptors in nematodes.";
Submitted (UUN-2001) to the EMBL/GenBank/DDBJ databases.
R EMBL, AR87606; AR470489.1; --.
R GO; GO:0016020; C:membrane; IEA.
R GO; GO:0004984; F:olfactory receptor activity; IEA.
R GO; GO:0004872; F:receptor activity; IEA.
R GO; GO:0007608; P:olfaction; IEA.
R H FPO2949; 7tm_6; I. h Similarity 83.3%; Pred. No. 9.2; 5; Conservative 1; Mismatches 0; Indels 447 AA; 51176 MW; 3AB7B4216F048BEB CRC64; 01-DEC-2001 (TrEMBLrel. 19, Created) 01-DEC-2001 (TrEMBLrel. 19, Last sequence update) 01-OCT-2003 (TrEMBLrel. 25, Last annotation update) Putative chemoreceptor GUR-3. 447 AA PRT; PRELIMINARY; Local Similarity SEQUENCE FROM N.A. SEQUENCE Query Match Q963E7 GUR-3 Best Loca Matches RESULT 1 **2963E7** AC DT DT DD DD DD DD DD SQ

RESULT

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STRAIN=02TH OUR1331;
Pubmed=12908933;
Tovanabutra S., Watanaveeradej V., Viputtikul K., De Souza M.,
Razak M.H., Suriyanon V., Jittiwutikarn J., Sriplienchan S.,
Nitayaphan S., Benenson M.W., Sirisopana N., Renzullo P.O.,
Brown A.E., Robb M.L., Beyter C., Celentano D.D., McNeil J.G.,
Brown A.E., Robb M.L., McCutchan F.E.;
A New Circulating Recombinant Form, CRF15 01B, Reinforces the Linkage
between IDU and Heterosexual Epidemics in Thailand.";
AIDS Res. Hum. Retroviruses 19:561-567(2003).
EMBL, AF529572; AAQ09553.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                           Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
NCBI_TaxID=6239;
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                                                                                                                                                                                                                                                                                                                                                                                                                  97.4%; Score 37; DB 5; Length 447; ilarity 83.3%; Pred. No. 9.2; Conservative 1; Mismatches 0; Indels
                                                                                                                                                                                                                                              "Genome sequence of the nematode C.elegans: A platform for
                                                                                                                                                                            Kershaw J.K.;
Submitted (JUL-1995) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Envelope protein.
SEQUENCE 849 AA, 96536 MW, D7AB6F8B670BAED3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                    Pfam; PF02949; 7tm 6; 1. SEQUENCE 447 AA; 51227 MW; E916BEAA7C14C80C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-00T-2003 (TrEMBLrel. 25, Created)
01-00T-2003 (TrEMBLrel. 25, Last sequence update)
01-00T-2003 (TrEMBLrel. 25, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Viruses, Retroid viruses, Retroviridae, Lentivirus.
NCBI_TaxID=11676;
                                                                                                                                                                                                                                                                                                            WormPep; ZC504.5; CE30223.

GO; GO:00156020; C:membrane; IEA.

GO; GO:0005549; F:odorant binding; IEA.

GO; GO:0004984; F:olfactory receptor activity; IEA.

GO; GO:0007608; P:olfaction; IEA.

InterPro; IPR004117; 7tm_6.
                                                     Last sequence update)
Last annotation update)
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Pred. No. 16;
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                  447 AA.
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                 PRT;
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MEDLINE=99069613; PubMed=9851916;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           97.4%;
                                                                                                                                                                                                                                                          investigating biology.";
Science 282:2012-2018(1998).
EMBL; Z50029; CAA90343.3; -.
PIR; T27621; T27621.
                                        01-JAN-1998 (TrEMBLrel. 05, 01-MAR-2002 (TrEMBLrel. 20, 01-OCT-2003 (TrEMBLrel. 25,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
                  PRELIMINARY;
                                                                                                      Caenorhabditis elegans.
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                                                                             ZC504.5 protein.
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MEDLINE=21365705; PubMed=11472063;

MEDLINE=21365705; PubMed=11472063;

Sun P.C., Uppaluri R., Schmidt A.P., Pashia M.E., Quant E.C.,
Sunwoo J.B., Gollin S.M., Scholnick S.B.;

"Transcript map of the 8p23 putative tumor suppressor region.";
Genomics 75:17-25 (2001).

"In "Transcript map of the 8p23 putative tumor suppressor region.";
Genomics 75:17-25 (2001).

"In Genomics 75:17-25 (2001).

"ANOING STATE TY: CONTAINS 14 CUB DOMAINS.

"ANOING GOOGS PROBLOGO STATE METABOLISM; IEA.

"InterPro; IPRO000859; CUB.

"InterPro; IPRO000859; CUB.

"InterPro; IPRO000859; Sushi_SCR_CCP.

"Rem; PRO00100084; Sushi_SCR_CCP.

"Rem; PRO00184; Sushi; 25.

"Remar; SMORO12; CCP; 25.

"REMART; SMORO12; CUB; 14.

"REMART; SMORO12; CUB; 14.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                        Homo sapiens (Human).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                          Q9H4W4;
01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DJ947L8.1.8 (Novel sushi (SCR repeat) domain protein) (Fragment).
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Pred. No. 17;
1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                       Wallis J.;
Submitted (SEP-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; ALJS5178; CAC10283.1; -.
HSSP; P10998; 1VVD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      533 AA; 57921 MW; 0554F7E10911F9BF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          096QU9 PRELIMINARY; PRT; 3389 AA. 096QU9; OLDEC-2001 (TEMBLrel. 19, Created) 01-DEC-2001 (TEMBLrel. 19, Last sequence update) 01-DEC-2003 (TEMBLrel. 25, Last annotation update) 01-OCT-2003 (TEMBLrel. 25, Last annotation update) CUB and sushi multiple domains protein 1 short form. Homo sapiens (Human).
                                                                                                                     533 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Interpro, IPR000436; Sushi_SCR_CCP.
Pfam; PF00084; sushi; 8.
SMART; SM00032; CCP; 8.
                                                                                                                        PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     94.7%;
83.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity 83.3
Matches 5; Conservative
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125 CIPLTC 130
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94.78;
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les 5; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pfam; PF00001; 7tm_1; 1
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VARIANT
VARIANT
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Matches
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                                                                                                                                                                                                    Gaps
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Musinae, Mus.
NCBI_TaxID=10090,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens (Human).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sun P.C., Uppaluri R., Schnidt A.P., Pashia M.E., Quant E.C., Sunwo U.B., Gollin S.M., Scholnick S.B.;
Sunwoo U.B., Gollin S.M., Scholnick S.B.;
Genomics 75:17-25(2001).
-i - SINLIARITY: CONTAINS 14 CUB DOMAINS.
EMBL, AY017475; AAG54083.1;
MGD; MGI:2137383; CSMG1.
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Sun P.C., Uppaluri R., Schmidt A.P., Pashia M.E., Quant E.C.,
Sunwoo J.B., Gollin S.M., Scholnick S.B.;
"Transcript map of the 8p23 putative tumor suppressor region.";
Genomics 75:17-25 (2001).
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Pred. No. 88;
1; Mismatches 0; Indels 0
                                                                                                                            4; Length 3389;
                                                                                                                                                                                                    Indels
PROSITE; PS00591; GLYCOSYL HYDROL F10; 1.
SEQUENCE 3389 AA; 370293 MW; 53C3009FCD3ED76D CRC64;
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Last annotation update)
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Last annotation update)
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                                                                                                                     Score 36; DB
Pred. No. 84;
                                                                                                                                                                                                Mismatches
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InterPro; IPR000436; Sushi, SCR_CCP.
Pfam; PP00431; CUB; 14.
Pfam; PF000041; CUB; 14.
SMART; SM00032; CCP; 28.
SMART; SM00042; CUB; 14.
PROSITE; PS01180; CUB; 14.
SEQUENCE 3564 AA; 387865 MW; 7082.
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MEDLINE=21365705; PubMed=11472063;
                                                                                                                     94.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-DEC-2001 (TEMBLE1, 19, 01-DEC-2001 (TEMBLE1, 19, 01-OCT-2003 (TEMBLE1, 25,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  94.78;
                                                                                                                                                                                                Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mus musculus (Mouse)
                                                                           Query Match
Best Local Similarity
5; Conserve
                                                                                                                                                                                                                                                                                                                                        2677 CVPITC 2682
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Best Local Similarity
5; Conserv
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109231.3
AC 09231.3
AC 0
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296RM4
ID 096RM4
AC 096RM9
DT 01-0)
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Submitted (JUL-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; AF275536; AAG00977.1;
EMBL; AF275536; AAG00977.1;
EMBL; AL606722; CAR17596.1;
ZFIN; ZDB-GRNE-980526-16; ednrbl.
ZFIN; ZDB-GRNE-980526-16; ednrbl.
GO; GO:0016021; C:integral to membrane; IEA.
GO; GO:0016184; F:rhodopsin-like receptor activity; IEA.
GO; GO:0001786; P:G-protein coupled receptor protein signalin. .; IEA.
Interpro; JPR00075; GPCR_Rhodopsn.
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Johnson S.L.;
"Mutational analysis of roles for endothelin receptor bl during neural
crest and pigment pattern development in the zebrafish, Danio rerio.";
Submitted (JUN-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
Cyprinidae; Danio.
NCBI_TaxID=7955;
                                                                                                                                                                                                                                                                                                                                     Genew; HGNC:14026; CGND1...;

R GO; GO:0004553; F:hydrolase activity, hydrolyzing O-glycosyl . . .;

GO; GO:0004553; F:hydrolase activity, hydrolyzing O-glycosyl . . .;

R GO; GO:0005975; P:carbohydrate metabolism; IEA.

R InterPro; IPR001000; Glyco_hydro 10.

InterPro; IPR00436; Sushi_SCR_CCP.

R Pfam; PF00431; CUB; 14.

R PAMART; SM0042; CUB; 14.

R SMART; SM0042; CUB; 14.

R PROSITE; PS01180; CUB; 14.
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01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-07-2003 (TrEMBLrel. 25, Last annotation update)
Endothelin receptor bl (SI:dZ27N24.3) (Endothelin receptor B)
[2]
SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
SUN P.C., Uppaluri R., Schmidt A.P., Davis M.E., Quant B.C.,
Sun P.C., Uppaluri S.M., Scholnick S.B.,
Sunwoo J.B., Gollin S.M., Scholnick S.B.,
Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 36; DB 4; Length 3566;
Pred. No. 88;
1; Mismatches 0; Indels
                                                                                                                                                                                                       SEQUENCE FROM N.A.

Tong B., Scholnick S.B.;
Submitted (JAN-2003) to the EMBL/GenBank/DDBJ databases
EMBL; AFS333704; AAK73475.2; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Brachydanio rerio (Zebrafish) (Danio rerio).
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PROSITE; PS00237; G PROTEIN RECEP_F1_1;
PROSITE; PS50262; G_PROTEIN_RECEP_F1_2;
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A -> E.
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MEDLINE=21456161; PubMed=11572484; Magase T., Kikuno R., Ohara O.; "Prediction of the coding sequences of unidentified human genes. XXI. The complete sequences of 60 new cDNA clones from brain which code for
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                Length 578;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         92.1%; Score 35; DB 4; Length 946; 83.3%; Pred. No. 46; ive 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE 946 AA; 102543 MW; EDC903C6BD390B4A CRC64;
                                                                                                                                                                                           578 AA; 64140 MW; C9F6DA810133FED7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-DEC-2001 (TrEMBLrel. 19, Last sequence update) 01-MAR-2003 (TrEMBLrel. 23, Last annotation update) Hypothetical protein KIAA1884 (Fragment).
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                                                                                                                                                                                                                                                                                                     0;
                                                                                                                                                                                                                                             92.1%; Score 35; DB 11;
83.3%; Pred. No. 30;
tive 1; Mismatches 0;
GO, GO:0030154; P:cell differentiation; IEA. InterPro; IPR00800; Notch dom. InterPro; IPR00436; Sushi_SCR_CCP. Pfam, PR0064; sushi; 5. SWART; SM00032; CCP, 4. SWART; SM00004; NL; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT; 1367 AA
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01-DEC-2001 (TrEMBLrel. 19, Last seq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Large proteins.";
DNA Res. 8:179-187(2001).
EMBL, ABG67471; BAB67777.1;
InterPro; IPR000456; Sushi_SCR_CCP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PFEMN, PFO0064, BUBHI; 12.
SMART, SM00032; CCP; 12.
PROSITE, PS00290; IG_MHC; 1.
Hypothetical protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                5; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                      361 CVPVTC 366
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Matches 5; Conserv
                                                                                                                                                                                                                                                                         Local Similarity
nes 5; Conserv
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47 CVPVTC 52
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01-MAR-2001
                                                                                                                                                                                              SEQUENCE
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                                                                                                                                                                                                                                                   Query Match
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Matches
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Q9ES06
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN-C57BL/60; TISSUE-Embryo;
Olesen C., Hansen C., Hayashizaki Y., Byskov A., Tommerup N.;
Olesen C., Hansen C., Hayashizaki Y., Byskov A., Tommerup N.;
Partial sequence of Mus musculus Mus musculus pregnancy-associated
plasma protein A (Pappa).";
Submitted (Apr.-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AF260433; AAF70319.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
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01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
BM423P8.2 (Pregnancy-associated plasma protein A) (Fragment).
PAPPA.
                                                                                 92.1%; Score 35; DB 13; Length 426; 83.3%; Pred. No. 23; 1: Mismatches 0; Indel8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     92.1%; Score 35; DB 11; Length 468; 83.3%; Pred. No. 25;
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Submitted (OCT-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AL691454; CAD62274.1; -.
GO; GO:0016020; C:membrane; IEA.
        318 318 W -> *.
426 AA; 48770 MW; F92COBDB3046E4A3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      468 AA; 51134 MW; 85768E10D7D34FDA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                   01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last amnotation update)
Pregnancy-associated plasma protein A (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MGD; MGI:97479; Pappa.

GO; GO:0016020; C:membrane; IEA.

GO; GO:0030154; P:Cell differentiation; IEA.

InterPro; IPR000800; Notch dom.

InterPro; IPR000436; Sushi_SCR_CCP.

Pfam; PR00084; sushi; S.

SMART; SM00032; CCP; 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           578 AA
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01-JUN-2003 (TrEMBLrel. 24, Last seq
01-OCT-2003 (TrEMBLrel. 25, Last ann
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                                                                                                                                                                                                                                                                                                                                                                                      PRT;
                                                                                                            Local Similarity 83.3
les 5; Conservative
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SEQUENCE
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SEQUENCE
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Indels

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1; Mismatches Score 35; Pred. No.

DB 11; Length 1545; 70;

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Pfam; PF00084; sushi; 5.
SMART; SM00032; CCP; 4.
SMART; SM00066; LamGL; 1.
SMART; SM00004; NL; 3.
PROSITE; PS00112; ZINC_PROTEASE; 1.
NON_TER 1 1 1.
SEQUENCE 1545 AA; 172584 MW; B820BF9998245419 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 83.3%;
Matches 5; Conservative
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nes 5; Conserv
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SEQUENCE
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Q8R4K7
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RA SEQUENCE FROM N.A.

RA Haaning J., Sottrup-Jensen L., Haaning J., Gludice L.C., Conover C.A.,

RA Haaning J., Sottrup-Jensen L., Haaning J., Gludice L.C., Conover C.A.,

RA Maning J., Sottrup-Jensen L., Haaning J., Gludice L.C., Conover C.A.,

RA Maning J., Sottrup-Jensen L., Haaning J., Gludice L.C., Conover C.A.,

RA MEXING T., Incompany of recombinant murine PAPP-A and a novel variant (PAPP-Ai)

RI Expression of recombinant murine PAPP-A and a novel variant (PAPP-Ai)

RI Expression of recombinant murine PAPP-A and a novel variant (PAPP-Ai)

RI Expression of recombinant murine PAPP-A and a novel variant (PAPP-Ai)

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                                                                                   Hourritz A., Kuwahara A., Hennebold J.D., Negishi H., Tanaka M., Widger A., Erickson G.F., Adashi E.Y.; "The regulated expression of invalin-like growth factor binding protein-4-endopeptidase (Pregnancy-associated plasma protein-A) in the redent ovary: A marker of the dominant follicle and of the corpus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
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                                                                                                                                                                                                                                                                                                                                                         EMBL; AF258461; AAG09799.1; -. BMBL/GenBank/DDBJ databases.

R MEMCPS; Med. 6.001; -. McG. 6.001; -. McGD, MGI:97479; Pappa.

GO; GO:0018237; F:metallopeptidase activity; IEA.

GO; GO:0008270; F:metallopeptidase activity; IEA.

R GO; GO:00006508; P:cell differentiation, IEA.

R GO; GO:0006508; P:proteolysis and peptidolysis; IEA.

R InterPro; IPR000875; Peptidase_M43B.

R InterPro; IPR000875; Peptidase_M43B.

R InterPro; IPR000875; Peptidase_M43B.

R InterPro; IPR000875; Peptidase_M46; I.

R Pfam; PF00084; Sushi; 5.

R SMART; SM00032; CCP; 4.

SMART; SM00004; ML; 3.
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SEQUENCE FROM N.A.
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                                                      STRAIN=C57BL/6J;
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SEQUENCE
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0884K8
AC Q8R4K4
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DT
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    REPRESENTATIONS OF REPRESENTATIO
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"Expression of recombinant murine PAPP-A and a novel variant (PAPP-Ai)
"Expression of recombinant murine PAPP-A and a novel variant (PAPP-Ai)
with disferential proteolytic activity.";
Eur. J. Blochem. 0:0-0(2002).
EMBL; AF49514; AAM12688.1;
MGD; MGI:97479; Pappa.
                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
Soe R., Overgaard M.T., Thomsen A.R., Laursen L.S., Olsen I.M.,
Haaning J., Sottrup-Jensen L., Haaning J., Giudice L.C., Conover C.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus.
NCBI_TaxID=10090;
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01-UNY-2002 (TrEMBLrel. 21, Created)
01-UNY-2002 (TrEMBLrel. 21, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Pregnancy-associated plasma protein-A variant (Fragment)
PAPPA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1574 AA; 176105 MW; AE53F0187E6EFB7B CRC64;
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GG; GG:001620; C:nembrane; IEA.
GG; GG:000827; F:netallopeptidase activity; IEA.
GG; GG:0008270; F:netallopeptidase activity; IEA.
GG; GG:0008270; F:netallopeptidase activity; IEA.
GG; GG:0006508; P:proteolysis and peptidolysis; IEA.
GG; GG:0006508; P:proteolysis and peptidolysis; IEA.
InterPro; IPR006898; Comal like lec_gl.
InterPro; IPR006858; Lang like.
InterPro; IPR006874; Peptidase M43B.
InterPro; IPR006025; Peptidase M43B.
InterPro; IPR0060436; Sushī SCR CCP.
Ffam; PP05572; Peptidase M46; I.
Ffam; PP0084; Sushi; 5.
SMART; SM0056; Langli; 1.
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PROSITE; PS00142; ZINC_PROTEASE; 1.
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Q7Z408;
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ID Q7
AC Q7
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DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE CUB and sushi multiple domains 2.
GN CSMD2.
GN Manmalla; Eucheria; Primates; Catarrhini; Hominidae; Homo.
OC Manmalla; Eucheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBL TaxID=9606;
RN 11
RP SEQUENCE FROW N.A.
RN MEDLINE=22788796; PubMed=12906867;
RA ADUNIS, Scholnick S.B.;
RY MEDLINE=22788796; PubMed=12906867;
RA Lau W.L., Scholnick S.B.;
RY Genomics 82:412-415(2003).
DR REMBL; AX210418; AA034701.1; -.
SQ SEQUENCE 3487 AA; 380035 MW; 3A77D8457DF8EFB5 CRC64;
Ouery Match
Sy Conservative 1; Mismatches 0; Indels 0; Gaps
Oy 1 CVPLTC 6
UP 11 | | | | |
Db 2588 CVPVTC 2593
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Search completed: September 5, 2004, 10:00:05 Job time: 15.5758 secs

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5, 2004, 09:37:49; Search time 19.697 Seconds (without alignments) 86.068 Million cell updates/sec
 5.1.6
Compugen Ltd.
                                                                                                                                                                                                                                                               1586107 segs, 282547505 residues
GenCore version
Copyright (c) 1993 - 2004
                                                       OM protein - protein search, using sw model
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                                                                                                                                                   US-09-761-636A-12
38
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                                                                                                                                                                     Perfect score:
                                                                                                                                                                                                                   Scoring table:
                                                                                                                                                                                    Sequence:
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Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries geneseqp1990s:*
geneseqp2000s:*
geneseqp2001s:* geneseqp2002s:* geneseqp2003as:* A_Geneseq_29Jan04:* geneseqp2003bs:*geneseqp2004s:* geneseqp1980s:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

1		₩ (SUMMARIES	
No.	Score	Query	Length	DB	ID	Description
4	38	100.0	9	4	AAU04531	2011 07 07 15 31 0 0 1 1 2 1 1 1 1 1 1 1 1 1 1 1 1 1 1
7	36	94.7	144	Ŋ	ABB53096	
٣	36	94.7	613	4	AATTOORIA	Human
4	36	4	882	4	AAB83372	
Ŋ	36	4	883	4	AAB83371	NOVIE
Q	36	94.7	3069	Ŋ	AAE20787	
7	36	94.7	3069	ß	AAE20900	Time II
œ	36	94.7	3095	Ŋ	AAE20788	Dat 40
σ	36	94.7	3100	2	AAE20789	Enancia Enancia
10	36	94.7	3100	Ŋ	AAE20901	Ase 20001 Usuman CSD
11	36	94.7	3104	Ŋ	ABG79168	Human
12	35	92.1	95	4	AAU48199	
13	35	92.1	95	9	ABM44718	Abm44719 Bronionib
14	32	92.1	310	9	ADA55489	
15	35	92.1	368	7	ADD27716	
16	35	92.1	530	7	ADD46650	
17	35	92.1	530	7	ADE55158	Adelete Prote
18	35	92.1	1603	4	AAU32498	
19	35	92.1	1752	4	ABG11138	Novel
20	34	89.5	570	7	ADB65688	INC.
21	33	86.8	10	"	AAB23798	
22	33	86.8	09	4	AA1140081	Filage
23	33	86.8	09	4	AAUG225	Aguatoda Fropionio
24	33	86.8	9	9	ABM36600	
25	33	86.8	9	9	ABM62744	Abm62744 Propionib

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ABP29076	AAU67640	ABM64159	ABM64758	ADT11 CE 0-1	TECOTOGU	ADA33421	AAU55878	ABM52397	ABB82487	00000000	AA125004	AAP80361	ABB604R0	0171744	AAII3438	ABR58468	AAB40917	AAM50361	ABDEGACT	(DE00 VITE	ADA57157	ADA41023	000000000000000000000000000000000000000	AA191362
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26	27	28	29	30		7 1	32	33	34	3.5) (36	37	æ	0 0	υ. υ.	40	41	42		4.	44	45)

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Total number of hits satisfying chosen parameters:

length: 0 length: 2000000000

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Minimum I Maximum I

Human; VEGF; vascular endothelial growth factor; angiogenesis; neovascularisation; lymphangiogenesis; psoriasis; tumour; diabetes induced neovascular sequelae; rheumatoid arthritis; diabetic retinopathy; chronic inflammation; cyclic. AAU04531 standard; peptide; 6 AA. VEGF based monocyclic peptide 9. (first entry) 26-SEP-2001 Synthetic. AAU04531; AAU04531 ID AAU(

Location/Qualifiers
1. .6
/note= "This bond cyclises the peptide" Key Disulfide-bond

18-JAN-2000; 2000US-0176293P. 16-MAY-2000; 2000US-0204590P. 18-JAN-2001; 2001WO-US001533. WO200152875-A1. 26-JUL-2001.

Cendron A; Stacker S, Hughes RA, WPI; 2001-442248/47. Achen MG,

(LUDW-) LUDWIG INST CANCER RES.

Novel monomeric monocyclic peptide, used to interfere with angiogenesis, or lymphangiogenesis, is produced by cyclizing a peptide loop fragment from an exposed loop of a growth factor protein by oxidizing the cysteine residues.

Claim 49; Page 32; 102pp; English.

The sequence represents a monomeric monocyclic peptide of the invention, whose 3-dimensional structure is modelled on the expose loop of human VEGFD (vascular endothelial growth factor). The invention relates to a method of producing a monomeric monocyclic peptide by a measuring betabeta carbon separation distances on opposite antiparallel strands of a

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peptide loop fragment from an exposed loop of a growth factor protein and cyclising the peptide by oxidising the cysteine residues. The monocyclic peptides, dimeric bicyclic peptides (comprising 2 linked monocyclic peptides) and a cyclic peptide with at least one amino acid deleted prior to cyclisation are used to interfere with anglogenesis, to cyclisation are used to interfere with anglogenesis.

The condition is diabetic retinopathy, psoriasis, arthropathy carefularisation or lymphangiogenesis, newscularisation or lymphangiogenesis.

The condition is diabetic retinopathy, psoriasis, arthropathy, cerebrovascular accident, post-angioplasty restenosis, head, heat or cold trauma, substance-induced neovascularisation of the liver, excessive trauma, substance-induced neovascularisation of the liver, excessive cramma, the peptides are also used to modulate vascular permeability in a mammal (the mammal has a condition characterised by fluid accumulation in peripheral limbs or in lungs, peritoneal cavity, pleura, or brain. The peptides are used to inage blood vessels and lymphatic or brain. The peptides are used to inage blood vessels and lymphatic or brain. The peptides are also used to wearly selective to treat a chronic inflammation, especially rheumatoid arthritis, psoriasis and discord are also used in combination with an anti-inflammatory agent, to treat a chronic inflammation, especially rheumatoid arthritis, psoriasis and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORFX; human; pharmacogenomics; cancer; hyperproliferative disorder; dysproliferative disorder; neurodegenerative disorder; organ transplant; cardiovascular disease; cytokine; cell proliferation; immunomodulatory; cell differentiation; haematopoiesis; tissue growth; thrombolytic; nootropic; neuroprotective; antiarthritic; antimicrobial; vulnerary; cytostatic; antidiabetic; virucide; antiinfertility; anticonvulsant; amostropic; antidiabetic; virucide; antiinfertility; anticonvulsant; antiulcer; osteopathic; tranguliser; cerebroprotective; hepatotropic; antinflammatory; tumour inhibition.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100.0%; Score 38; DB 4; Length 6;
100.0%; Pred. No. 1.4e+06;
ive 0; Mismatches 0; Indels
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05-APR-2001; 2001US-00826734.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     06-APR-2001; 2001WO-US040469.
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N-PSDB; ABA90195.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  diabetic retinopathy
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Matches 6; Conserv
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ABB53096
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Gaps . 0

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New polypeptides and polynucleotides, useful for treating diseases such as cancer, Alzheimer's disease, atherosclerosis, diseases associated with liver, comprises polypeptides and polynucleotides of open reading frame
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                                                                                                                                                                                                  The present invention provides the protein and coding sequences of human OREX, where X is any number between 1 and 132. These sequences can be used to diagnose and treat OREX related disorders, including cancer, hyperproliferative and dysproliferative disorders, incurdegenerative disorders, disorders, disorders call to organ transplantation or cardiovascular diseases, and may have cell proliferation or differentiation, cytokine, immunomodulatory, haematopoiesis regulating, tissue growth, inhibin or activin, chemotactic or chemokinetic, haemostatic or thrombolytic and/or antinflammatory activities. The present sequence is one of the OREX
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/label= Immunoglobulin_like_domain
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/label= Immunogenic_epitope
328. .386.
/label= Immunogenic_epitope
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|abel= Immunogenic_epitope
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/label= Immunogenic_epitope
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/label= Immunogenic_epitope
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAU00816 standard; protein; 613 AA
                                                                                                                                                          Claim 11; Page 82; 111pp; English.
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/label= Im-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 144 AA;
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Region

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Isolated nucleic acid molecule encoding a human secreted protein is used in preventing, treating or ameliorating a medical condition.
         484. .500
/label= Immunogenic_epitope
 /label= Immunogenic_epitope
                              /label= Immunogenic_epitope
                                    577. 583
/label= Immunogenic_epitope
                                                         /label= Immunogenic_epitope
                                                                                                                                                                                                            Claim 11; Page 238-239; 247pp; English.
                                                                                                                                                                                       Isolated nucleic acid molecule
                                                                                                  29-AUG-2000; 2000WO-US023662.
                                                                                                                 99US-0152248P.
                                                                                                                              (HUMA-) HUMAN GENOME SCI INC. (NIJJ/) NI J.
                                                   .610
                      517
                                                                                                                                                     Ruben SM,
                                                                                                                                                                  WPI; 2001-203084/20.
                                                                                                                                                                          N-PSDB; AAS00146.
                                                                                                                                                                                                                                                                                                                                                                                     Sequence 613 AA;
                                                                        WO200118176-A1.
                                                                                                                 03-SEP-1999;
                                                                                     15-MAR-2001
                                                                                                                                                     Young PE,
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The sequence is a Human Immunoglobulin superfamily, IgSF, protein, a diverse family of proteins involved in cell-cell interactions, cell-cal verse family of proteins involved in cell-cell interactions, cell-cal inflammatory responses. Polypeptides and antibodies directed to polypeptides of the present invention are useful to provide immunological probes for differential identification of tissues. Antibodies can be used to assay levels of polypeptides encoded by polymuclectides of the invention. Polypeptides of the present invention can be used to treat or disorders, muscular disorders, immune system disorders, pulmonary disorders, reproductive disorders, immune system of sorders, proliferative disorders, and/or cancerous diseases and disorders, proliferative disorders, and/or cancerous diseases and conditions. Polymuclectides of the invention are also useful in treating the above disorders. Examples of the disorders include common variable adhesion deficiency syndrome, acquired immunodeficiency syndrome (C anaemia, rheumatoid arthritis, Alzheimer's disease, Crohn's disease, C liver cancer, leukaemia, Hodgkin's lymphoma, parkinson's disease, dementia, artherosclerosis, stroke, diabetes conditions, Addison's disease, urticaria, severe combined immunodeficiency (SCID). Many more examples of diseases and disorders are given in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity
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94.7%; Score 36; DB 4; Length 613; 83.3%; Pred. No. 6.7e+02; ive 1; Mismatches 0; Indels
                             5; Conservative
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Matches
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|||:|| 264 CVPITC 269 RESULT

AAB83372 standard; protein; 882 AA. 26-MAR-2002 (first entry) NOV16 protein sequence. AAB83372; AABB3372
ID AABB
XX
AC AABE
XX
DT 26-N
XX
DE NOVI

NOV, Cytostatic; contraceptive; antiinflammatory; immunomodulatory; cardiovascular; casein kinase II phosphorylation site; contraception; serine/threonine kinase. Peutz-Jeghers syndrome; cellular proliferation; epidermal growth factor; cell development; apoptosis; cell adhesion; growth migration; cell structure; motility; cancer; immune disorder; diffarmatory disorder; cellular adhesion disorder; long-QF syndrome; cardiovascular disease; hypertrophic cardiomyopathy; marfan syndrome; therapy; NOV1; NOV2; NOV4; NOV5; NOV6; NOV7; NOV9; NOV9; NOV10;

Unidentified.

WO200136638-A2.

25-MAY-2001

17-NOV-2000; 2000WO-US031543

19-NOV-1999; 99US-0166336P. 29-NOV-1999; 99US-0167785P. 08-MAR-2000; 2000US-0187844P. 16-NOV-2000; 2000US-00715417

(CURA-) CURAGEN CORP.

щ Fernandes Vernet C, Shimkets RA, Lichenstein H,

WPI; 2001-648134/74. N-PSDB; AAF87127. Novel human polypeptides and the nucleic acids that encode them useful for preventing, diagnosing and treating e.g. cancer, inflammation and for preventing, di immune disorders.

Claim 1; Page 50-52; 141pp; English.

Cutivities. The sequences may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate NOVX expression. They be used to treat disorders associated with inappropriate NOVX expression. They are used to treat disorders associated with decreased expression. They crectifying mutations or deletions in a patient's genome that affect the activity of protein by expressing inactive proteins or to supplement the patients own production of protein. They are used to produce NOVX patients own production of protein. They are used to produce NOVX creativity of protein. The DNA may be used as DNA probes in assays to detect and quantitate the presence of similar DNAs in samples, and which patients may need restorative therapy. The NOVX protein may also be used as antigens in the production of antibodies (Abs) against NOVX and in assays to identify modulators of NOVX expression and activity. The anti-NOVX Abs are used to down regulate expression and activity. The anti-NOVX Abs are used to down regulate expression and activity. The anti-NOVX Abs are used for detecting the presence of NOVX in samples. Disorders that may be prevented, diagnosed and/or treated contractive the norm of NOVX in samples. Disorders that may be prevented, diagnosed and/or treated contractive the norm of NOVX in samples. The NOVX protein. NOVI, NOV3, NOV5, NOV7, NOV9-11 and NOV13-16 have casein kinase in phosphorylation sites characteristic of contractive. NOV16 proteins, and their coding sequences. The proteins have Cytostatic; contraceptive; antiinflammatory; immunomodulatory; and cardiovascular (e.g. Peutz-Jeghers syndrome, cellular proliferation and contraception). MoV2-3, NOV6 and NOV9 are homologous to the epidermal growth factor (EGF) like Super family and are involved in, e.g. regulation of cell development, apoptosis, cell addhesion, growth migration, cell structure and motility and protein management, and are used to treat cancers, inflammatory disorders, immune disorders and cellular adhesion disorders. serine/threonine kinases, and are used to treat kinase-related disorders NOV6-10 are homologous to EGF-like fibrillin proteins and are used to treat cardiovascular disease e.g. hypertrophic cardiomyopathy, long-QT This sequence is the NOV16 protein. The invention relates to the NOV1syndrome and marfan syndrome

Sequence 882 AA;

Gaps . 0 Score 36; DB 4; Length 882; Pred. No. 9.2e+02; 1; Mismatches 0; Indels 1; 94.7%; 83.3%; 5; Conservative Best Local Similarity Matches 5; Conserva Query Match

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(e.g. Peutz-Jeghers syndrome, cellular proliferation and contraception). NOV2-3, NOV6 and NOV8 are homologous to the epidermal growth factor (EGF) like super family and are involved in, e.g. regulation of cell development, apoptosis, cell adhesion, growth migration, cell structure and motility and protein management, and are used to treat cancers, inflammentory discorders, immune disorders and cellular adhesion disorders. NOV6-10 are homologous to EGF-like fibrillin proteins and are used to treat cardiovascular disease e.g. hypertrophic cardiowyopathy, long-OT

syndrome and marfan syndrome

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Sequence 883 AA;

Query Match

Length 883;

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NOV; Cytostatic; contraceptive; antiinflammatory; immunomodulatory; cardiovascular; casein kinase II phosphorylation site; contraception; serine/threonine kinase; Peutz-Jeghers syndrome; cellular proliferation; epidermal growth factor; cell development; apoptosis; cell adhesion; growth migration; cell structure; motility; cancer; immune disorder; inflammatory disorder; cellular adhesion disorder; long-OT syndrome; cardiovascular disease; hypertrophic cardiomyopathy; marfan syndrome; therapy; NOV1; NOV2; NOV4; NOV4; NOV6; NOV6; NOV9; NOV9; NOV10;
                                                                      AAB83371 standard; protein; 883 AA.
                                                                                                                                                                                                                                                                                                                                        19-NOV-1999; 99US-0166336P.
29-NOV-1999; 99US-0167785P.
08-MAR-2000; 2000US-0187844P.
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                                                                                                                                                                                                                                                                                                                      17-NOV-2000; 2000WO-US031543.
                                                                                                                                                                                                                                                                                                                                                                        16-NOV-2000; 2000US-00715417
                                                                                                             (first entry)
                                                                                                                                  NOV15 protein sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2001-648134/74.
                  264 CVPITC 269
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CVPLTC 6
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                                                                                                                                                                                                                                                                             WO200136638-A2.
                                                                                                                                                                                                                                                           Unidentified.
                                                                                                                                                                                                                                                                                                                                                                                                                Shimkets RA,
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                                                                                                             26-MAR-2002
                                                                                          AAB83371;
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                                                             AAB8337
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Claim 13; Fig 1; 251pp; English
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                                                                                                                                                                                                                                                                                                                  Misc-difference 586
                                                                                                                                                                                                                        Misc-difference 461
                                                                                                                          Misc-difference 387
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AMGE-) AMGEN INC.
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Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Welcher AA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     07-FEB-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This sequence is the NOV15 protein. The invention relates to the NOV1-
NOV16 proteins, and their coding sequences. The proteins have Cytostatic;
NOV16 proteins, antihifammatory; immunodulatory; and cardiovascular
activities. The sequences may be used in the prevention, diagnosis and
treatment of diseases associated with inappropriate NOVX expression. They
may be used to treat disorders associated with decreased expression. Dy
certifying mutations or deletions in a patient's genome that affect the
activity of protein by expressing inactive proteins or to supplement the
activity of protein by expressing inactive proteins or to supplement the
patients own production of protein. They are used to produce NOVX
proteins, by inserting the nucleic acid into a cell and culturing it to
express the protein. The DNA may be used as DNA probes in assays to
detect and quantitate the presence of similar DNAs in samples, and which
as antigens in the production of antibodies (Abs) against NOVX and in
assays to identify modulators of NOVX expression and activity. The anti-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NOVX Abs and antegonist are used to down regulate expression and activity. The anti-NoVX Abs are used for detecting the presence of NOVX in samples. Disorders that may be prevented, diagnosed and/or treated vary depending on the NOVX protein. NOV1, NOV3, NOV5, NOV7, NOV9-11 and NOV13-16 have casein kinase II phosphorylation sites characteristic of serine/threonine kinases, and are used to treat kinase-related disorders
                                                                                                                                                                                                                                                                                                                       Novel human polypeptides and the nucleic acids that encode them useful for preventing, diagnosing and treating e.g. cancer, inflammation and
                                                                                              Vernet C, Fernandes E;
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                                                                                                                                                                                                                                              Human, C3b/C4b complement receptor-like molecule; immune system disorder; gene therapy; rheumatoid arthritis; psoriatic arthritis; osteoarthritis; inflammatory arthritis; inflammatory joint disease; Alzheimer's disease; unflammatory arthritis; inflammatory bowel disease; nervous system disorder; transplant rejection; autoimmune disease; ischaemic condition; motoropic; metabolic disorder; immunomodulatory; neuroprotective; diabetes; lupus; infertility; vasodilator; obesity; cardiant.
                            Gaps
                            ..
                          0; Indels
                                                                                                                                                                                                                         Human C3b/C4b complement receptor like protein #1.
Score 36; DB 4; 1
Pred. No. 9.2e+02;
1; Mismatches 0;
                                                                                                                                             AAE20787 standard; protein; 3069 AA.
                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                        label= Unknown
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2000US-00728787
                83.3%;
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              Local Similarity 83.3
hes 5; Conservative
                                                                            264 CVPITC 269
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The invention relates to a nucleic acid encoding a novel G3b/C4b

Complement receptor (CR)-like nucleic acid molecule. The C3b/C4b CR-like

polypeptide and nucleic acid molecules may be used to treat, prevent,
ameliorate, diagnose and/or detect diseases such as immune system

disorders such as rheumatoid arthritis, psoriatic arthritis, inflammatory
arthritis, osteoarthritis, inflammatory joint disease, autoimmune

clisease, multiple sclerosis, lupus, inflammatory bowel disease,
transplant rejection, nervous system disorders (e.g. Alzheimer's

disease), ischaemic conditions, metabolic disorders (e.g. Alzheimer's

disease) infertility. The invention is useful in gene therapy. The

present sequence is human C3b/C4b complement receptor like protein. Note:

The present sequence is stated to be the same as that referred to as SEQ

ID NO:2 (AAE20900) shown in page 176-189 of the specification. However
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human, C3b/C4b complement receptor-like molecule; immune system disorder; gene therapy; rheumatoid arthritis; psoriatic arthritis; osteoarthritis; inflammatory inflammatory joint disease; Alzheimer's disease; multiple sclerosis; inflammatory bowel disease; nervous system disorder; transplant rejection; autoimmune disease; ischaemic condition; nootropic; metabolic disorder; immunomodulatory; neuroprotective; diabetes; lupus; infertility; vasodilator; obesity; cardiant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human C3b/C4b complement receptor like protein #1, alternative version.
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Pred. No. 2.8e+03;
1; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                  94.7%;
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Best Local Similarity 83.3%,
Fac 5; Conservative
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                                                                                                                                                                                                                                                  Sequence 3069 AA;
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The invention relates to a nucleic acid encoding a novel C3b/C4b complement receptor (CR)-like nucleic acid molecule. The C3b/C4b CR-like Complement receptor (CR)-like nucleic acid molecules may be used to treat, prevent, ameliorate, diagnose and/or detect diseases such as immune system disorders such as rheumatoid arthritis, psoriatic arthritis, inflammatory arthritis, psoriatic arthritis, inflammatory disease, autoimmune conferes withing salerosis, lupus, inflammatory bowel disease, transplant rejection, nervous system disorders (e.g. Alzheimer's disease) ischaemic conditions, metabolic disorders (e.g. Alzheimer's catabolate for infertility. The invention is useful in gene therapy. The present sequence is human C3b/C4b complement receptor like protein, alternative version. Note: The present sequence is stated to be the same cas that referred to as SEQ ID NO:2 (AABE20787) shown in figure 1 of the specification. However the sequences differ at position 695
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                  Nucleic acid encoding a novel C3b/C4b Complement Receptor-like nucleic acid molecule, useful for treating, preventing and diagnosing rheumatoid arthritis, psioriatic arthritis, inflammatory arthritis, and multiple
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 gene therapy, rheumatoid arthritis, psoriatic arthritis, osteoarthritis, inflammatory arthritis; inflammatory joint disease, Alzheimer's disease, multiple sclerosis; inflammatory bowel disease, nervous system disorder; transplant rejection; autoimmune disease; ischaemic condition; nootropic; metabolic disorder; immunomodulatory; neuroprotective; diabetes; lupus; infertility; vasodilator; obesity; cardiant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Rat; C3b/C4b complement receptor-like molecule; immune system disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 3069;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 36; DB 5; Length 306
Pred. No. 2.8e+03;
1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             'note= "Xaa can be any amino acid"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Rat C3b/C4b complement receptor like protein.
                                                                                                                                        Claim 13; Page 176-189; 251pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAE20788 standard; protein; 3095 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /label= Unknown
/note= "Xaa can be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    24-JUL-2001; 2001WO-US023232.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     02-AUG-2000; 2000US-0222504P.
28-NOV-2000; 2000US-00728787.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        94.78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           83.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CVPITC 2243
WPI; 2002-303934/34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Misc-difference 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 CVPLTC 6
                    N-PSDB; AAD33318.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 3069 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WO200210199-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Rattus rattus.
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                                                                                                        sclerosis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2238
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
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The invention relates to a nucleic acid encoding a novel C3b/C4b complement receptor (CR)-like nucleic acid molecule. The C3b/C4b CR-like polypeptide and nucleic acid molecules may be used to treat, prevent, ameniotrate, diagnose and/or detect diseases such as immune system disorders such as rheumatoid arthritis, psoriatic arthritis, inflammatory arthritis, osteoarthritis, inflammatory joint disease, autoimmune disease, multiple sclerosis, lugus, inflammatory bowel disease, transplant rejection, nervous system disorders (e.g. Alzheimer's disease), ischaemic conditions, metabolic disorders (e.g. obesity and diabetes) and infertility. The invention is useful in gene therapy. The present sequence is rat C3b/C4b complement receptor like protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human, C3b/C4b complement receptor-like molecule; immune system disorder; gene therapy, rheumatoid arthritis; psoriatic arthritis; osteoarthritis; inflammatory dint disease; Alzheimer's disease; multiple sclerobis; inflammatory bowel disease; nervous system disease; transplant rejection; autoimmune disease; ischaemic condition; nootropic; metabolic disorder; immunomodularory; neuroprotective; diabetes; lupus; infertility; vasodilator; obesity; cardiant.
                                                                                                           Nucleic acid encoding a novel C1b/C4b Complement Receptor-like nucleic acid molecule, useful for treating, preventing and diagnosing rheumatoid arthritis, psioriatic arthritis, inflammatory arthritis, and multiple
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 36; DB 5; Length 309
Pred. No. 2.8e+03;
1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human C3b/C4b complement receptor like protein #2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAE20789 standard; protein; 3100 AA.
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                                                                                                                                                                                                   Claim 13; Fig 3; 251pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        24-JUL-2001; 2001WO-US023232.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        94.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5; Conservative
                               Welcher AA, Elliott GS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2264 CVPITC 2269
                                                                 WPI; 2002-303934/34.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 CVPLTC 6
AMGEN INC
                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 3095 AA;
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                                                                                    N-PSDB; AAD33319
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          07-FEB-2002.
                                                                                                                                                                       sclerosis.
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 (AMGE-)
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Length 3095;

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The invention relates to a nucleic acid encoding a novel C3b/C4b complement receptor (CR)-like nucleic acid molecule. The C3b/C4b CR-like polypeptide and nucleic acid molecules may be used to treat, prevent, amaliorate, diagnose and/or detect diseases such as immune system disorders such as rheumatoria arthritis, psoriatic arthritis, inflammatory arthritis, posteoarthritis, inflammatory joint disease, autoimmune disease, multiple sclerosis, lupus, inflammatory bowel disease, disease, ransplant rejection, nervous system disorders (e.g. Alzheimer's disease), ischaemic conditions, metabolic disorders (e.g. obesity and diabetes) and infertility. The invention is useful in gene therapy. The present sequence is stated to be the same as that referred to as SEQ ID NO:7 (AAE20901) shown in page 239-251 of the specification. However the sequences differ at position 726
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human, C3b/C4b complement receptor-like molecule; immune system disorder; gene therapy; rheumatoid arthritis; psoriatic arthritis; osteoarthritis; inflammatory arthritis; inflammatory joint disease; Alzheimer's disease; multiple solerosis; inflammatory bowel disease; nervous system disorder; transplant rejection; autoimmune disease; ischaemic condition; nootropic; metabolic disorder; immunomodulatory; neuroprotective; diabetes; lupus; infertility; vasodilator; obesity; cardiant.
                                                                                                                                                           Nucleic acid encoding a novel C3b/C4b Complement Receptor-like nucleic acid molecule, useful for treating, preventing and diagnosing rheumatold arthritis, psioriatic arthritis, inflammatory arthritis, and multiple
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human C3b/C4b complement receptor like protein #2, alternative version.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /label= Unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /label= Unknown
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                                                                                                                                                                                                                                                     Claim 13; Fig 2; 251pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          94.7%;
83.3%;
2000US-0222504P.
2000US-00728787.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5; Conservative
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                                                                                    Elliott
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                                                                                                                   2002-303934/34.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 3100 AA;
                                                    (AMGE-) AMGEN INC.
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                                                                                                                     WPI; 2002-303934,
N-PSDB; AAD33320
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   02-AUG-2000;
28-NOV-2000;
                                                                                     Welcher AA,
                                                                                                                                                                                                                         sclerosis.
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us-09-761-636a-12.open.rag

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The invention relates to a nucleic acid encoding a novel C3b/C4b

Complement receptor (CR)-like nucleic acid molecule. The C3b/C4b CR-like

Complement receptor (CR)-like nucleic acid molecule. The C3b/C4b CR-like

Dolypoptide and nucleic acid molecules may be used to treat, prevent,

ameliorate, diagnose and/or detect diseases such as immune system

disorders such as rheumatoid arthritis, psoriatic arthritis, inflammatory

carbritis, osteoarthritis, inflammatory joint disease, autoimmune

carbritis, osteoarthritis, inflammatory bowel disease,

transplant rejection, nervous system disorders (e.g. Alzheimer's

ciasease), ischaemic conditions, metabolic disorders (e.g. Alzheimer's

disease), ischaemic conditions, metabolic disorders (e.g. Abcheimer's

ciabetes, and infertility. The invention is useful in gene therapy. The

present sequence is human C3b/C4b complement receptor like protein,

alternative version. Note: The present sequence is stated to be the same

condition. However the sequences differ at position 726

specification. However the sequences differ at position 726
                                                                                                                                                                                                                                                                                                                                                                      Nucleic acid encoding a novel C3b/C4b Complement Receptor-like nucleic acid molecule, useful for treating, preventing and diagnosing rheumatoid arthritis, psioriatic arthritis, inflammatory arthritis, and multiple
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 13; Page 239-251; 251pp; English.
                                                                                                                                                    02-AUG-2000; 2000US-0222504P.
28-NOV-2000; 2000US-00728787.
                                                                                                           24-JUL-2001; 2001WO-US023232.
                                                                                                                                                                                                                                                                Elliott GS;
                                                                                                                                                                                                                                                                                                           2002-303934/34.
                                                                                                                                                                                                                         (AMGE-) AMGEN INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 3100 AA;
                                                                                                                                                                                                                                                                                                                                N-PSDB; AAD33320
                      WO200210199-A2
                                                                                                                                                                                                                                                             Welcher AA,
                                                                  07-FEB-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                           sclerosis.
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Gaps
                               ;
0
94.7%; Score 36; DB 5; Length 3100; 83.3%; Pred. No. 2.8e+03; 1. Mismatches 0; Indels
                           5; Conservative
            Local Similarity
                                                   1 CVPLTC 6
Query Match
                         Matches
                                                   à
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|||:||| | 2269 CVPITC 2274

ABG79168 standard; protein; 3104 AA. ABG79168; RESULT 11 ABG79168 MARKA KARAKA KAR

Human cub and sushi domain containing protein #1. (first entry) 15-NOV-2002

Parkinson's disease; Huntington's disease; neurological disorder; schizophrenia; manic depression; mental retardation; angina pectoris; cardiovascular disease; acute heart failure; mycocardial infarction; muscular disease; muscular disorder; retinal disease; photoreception; defafiness; keratinisation disorder; retinal disease; photoreception; immunological disorder; inflammatory disease; immune disease; diabetes; bacterial infection; fungal infection; protozoal infection; obesity; viral infection; reproductive system disorder; metabolic disturbance; workal infection; sushi; myelin, von willebrand factor; kielin; semaphorin; serine/threonine protein kinase; TGF-beta binding; mas proto-oncogene; ribonuclease pancreatic precursor; aminotransferase; Human; NOVX; neurodegenerative disease; Alzheimer's disease; anxiety;

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as a result of a single
                                                                                by Gly as a result of a single (SNP)"
                                                                   as a result of a single
tolloid-like 2; cysteine sulfinic acid decarboxylase SNP; single nucleotide polymorphism.
                                              by Thr (SNP)"
                                                                 by Ala
(SNP)"
                                                                                   /note= "Asp substituted
nucleotide polymorphism
                                             /note= "Ala substituted
                                                     nucleotide polymorphism
                                                               /note= "Val substituted
                                                                        nucleotide polymorphism
                               Location/Qualifiers
1027
                                                                                                                                            08-DEC-2000; 2000US-0254329P.
14-DEC-2000; 2000US-025648P.
15-MAX-2001; 2001US-0291037P.
08-UUN-2001; 2001US-0297173P.
08-UUN-2001; 2001US-0309258P.
29-AUG-2001; 2001US-0315639P.
                                                                                                                                10-DEC-2001; 2001WO-US048369
                                                                                                                                                                                     2001US-0326393P
                                                          misc_difference 1084
                                                                            misc difference 1362
                                      misc_difference
                                                                                                      WO200264791-A2.
                   Homo sapiens
                                                                                                                                                                                    01-OCT-2001;
                                                                                                                   22-AUG-2002
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Anderson DW, Burgess CE, Boldog FL, Casman SJ; inger SR, Ellerman K, Gerlach V, Gorman L, Grosse WM; mn JL, Kekuda R, Lepley DM, Li, L, Macdougall UR; a CEA, Peyman JA, Rastelli, Rieger DK, Shimkets RA; pytek KA, Stone DJ, Tchernev VT, Vernet CAM, Voss EZ; Alsobrook JP, Anderson Colman SD, Edinger SR, Ellerman A, Guo X, Herrmann JL, Kekuda R, Lepinato X, Herrmann CLA, Peyman JA, Ra Zhong M; Spytek Ka, Zhong H, Z

(CURA-) CURAGEN CORP.

WPI; 2002-643486/69. N-PSDB; ABS64375 New NOVX polypeptides and polynucleotides useful for treating or preventing e.g. neurodegenerative diseases, neurological disorders, cardiovascular diseases muscular diseases and disorders, or immunological diseases.

Claim 1; Page 13-14; 299pp; English.

The present invention relates to new NOVX polypeptides. The polypeptides, polypucleotides and antibodies are useful in the manufacture of a medicament for treating or preventing neurodegenerative diseases (e.g. C. Alzheimer's disease, Parkinson's disease, or Huntington's disease).

Alzheimer's disease, Parkinson's disease, or Huntington's disease).

C. Alzheimer's disease, Parkinson's disease (e.g. acute heart failure, comental retardation), cardiovascular diseases and disorders, retinal diseases (including those involving photoreception, dasforders, retinal diseases (including those involving photoreception, deaffness and keratinisation disorders, inflammatory and immune diseases, bacterial, fungal, protozoal and viral infections, and reproductive compands that modulate the NOVX protein activity or expression, as well as to treat disorders characterised by insufficient or excessive production of NOVX protein forms that have decreased or aberrant activity compared to NOVX wild type protein, such as diabetes, obseity, metabolic disturbances associated with chronic diseases and various cancers, infections designed and various daslibated activity compared to nove the protein, such as diabetes, obseity, metabolic disturbances associated with chronic diseases and various cancers, infections diseases and various dyslipidaemias. The nucleic activity companded to many the modulation of the companded of sequences of the invention may be used in chromosome mapping, identifying an individual from minute biological samples (tissue typing), and in forensic identification of a biological sample. The present amino acid sequence represents a NOVX protein of the invention Sequence 95 AA;

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Sequences AAU39105-AAU68017 represent Propionibacterium acnes immunogenic polypeptides. The proteins and their associated DNA sequences are used in the treatment, prevention and diagnosis of medical conditions caused by a cares. The disorders include SAPHO syndrome (synovitis, acne, bustulosis, hypertosis and osteomylitis), uveitis and endophthalmitis.

P. acnes is also involved in infections of bone, joints and the central rerous system, however it is particularly involved in the inflammatory lesions associated with acne vulgaris. A method for detecting the presence or absence of P. acnes in a patient comprises contacting a sample with a binding agent that binds to the proteins of the invention and determining the amount of bound protein in the sample. The polypeptides may be used as antigens in the production of antibodies polypeptides may be used as antigens in the production of antibodies specific for P. acnes proteins. These antibodies can be used to downregulate expression and activity of P. acnes polypeptides and therefore treat P. acnes infections. The antibodies may also be used as diagnostic agents for determining P. acnes presence, for example, by contained in electronic format directly from WIPO at this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at
                                                                                                                                                                                                                                                                                                                                                                            SAPHO syndrome; synovitis; acne; pustulosis; hypertosis; osteomyelitis; uveitis; endophthalmitis; bone; joint; central nervous system; ELISA; inflammatory lesion; acne vulgaris; enzyme linked immunosorbent assay; dermatological; osteopathic; neuroprotectant.
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                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Propionibacterium acnes polypeptides and nucleic acids useful for vaccinating against and diagnosing infections, especially useful treating acne vulgaris.
                                                                    .
                              Score 36; DB 5; Length 3104;
Pred. No. 2.8e+03;
1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bhatia A;
                                                                                                                                                                                                                                                                                                                                              Propionibacterium acnes immunogenic protein #9095.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mitcham JL, Wang S
Jen S, Carter D;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Example 1; SEQ ID NO 9394; 1069pp; English.
                                                                                                                                                                                                                                       AAU48199 standard; protein; 95 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         20-APR-2001; 2001WO-US012865.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         21-APR-2000; 2000US-0199047P.
02-JUN-2000; 2000US-0208841P.
07-JUL-2000; 2000US-0216747P.
                                  94.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Persing DH, M
                                                                                                                                                                                                                                                                                                             27-FEB-2002 (first entry)
                 Propionibacterium acnes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2001-616774/71.
                                                                                                                               2486 CVPITC 2491
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                                                                                                            1 CVPLTC 6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         maisonneuve J,
Sequence 3104 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO200181581-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Skeiky YAW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-NOV-2001
                                                                                                                                                                                                                                                                           AAU48199;
                                                                                                                                                                                                  RESULT 12
                                                                                                                                                                                                                         AAU48199
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concoling a Propionibacterium acnes protein. The invention also relates to encoding a Propionibacterium acnes protein. The invention also relates to polypeptides encoded by the polynucleotides (ABM35624-ABM64536) and to immunogenic fragments of P. acnes polypeptides. The invention and to accompassion vectors and host cells comprising a diditionally encompasses expression vectors and host cells comprising a contention, fusion proteins comprising a polypeptide of the invention, a immune response specific for a P. acnes polypeptide and an isolated T cell population comprising T cells prepared collypeptide and an isolated T cell population comprising P. acnes polypeptides, via this method; a vaccine composition (comprising P. acnes polypeptides, or antigen-presenting cells that express the polypeptide); a method and kit for detecting or determining the presence or absence of P. acnes in a patient; and a method for inhibiting the development of P. acnes in a patient; and a method for inhibiting the development of P. acnes in collypeptides, polypucleotides, antibodies, fusion proteins, T cell populations or antigen-presenting cells that express the polypeptides are useful for diagnosing, preventing or treating acnes collypeptides are useful for diagnosing, preventing or treating acnes collypeptides can also be used as probes or primers for nucleic acid hybridisation. The vaccine composition is useful for the estimates of an immune response against P. acnes, or for treating acnes and the kit is useful for performing a diagnostic assay. The present conding frame) contained within the P. acnes polynucleotides of the
                                                        0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New Propionibacterium acnes polypeptides and polynucleotides encoding the polypeptide, useful for diagnosing, preventing or treating acne vulgaris, or for stimulating an immune response specific for a P. acnes protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The invention relates to an isolated polynucleotide (ACF64435-ACF64733)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Maisonneuve JL;
Jones R, Carter D;
                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                 Propionibacterium acnes predicted ORF-encoded polypeptide #9394.
                                                          ;
                                                                                                                                                                                                                                                                                                                                                                                                            vulgaris; antiseborrhoeic; dermatological; antibacterial;
                   Length 95;
                                                            0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bhatia A,
Benson DR,
                   92.1%; Score 35; DB 4; I
83.3%; Pred. No. 1.8e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Example 1; SEQ ID NO 9394; 1481pp; English
                                                            Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                      immunostimulant; immune response; vaccine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Persing DH,
Lodes MJ,
                                                                                                                                                                                                                                                   ABM44718 standard; protein; 95 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Zhang Y, Wang S, Jen S, Lod
Barth B, Vallieve-Douglass J;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     11-OCT-2002; 2002WO-US032727.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Skeiky YAW,
                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Propionibacterium acnes.
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Query Match
Best Local Similarity
Local 5; Conserve
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                                                                                                                                              CVPVTC 67
                                                                                                       1 CVPLTC 6
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                                                                                                                                                                                                                                                                                            ABM44718;
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(first entry)

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New complex of bait and prey between two polypeptides or polynucleotides encoding the two polypeptides of adipocytes, useful for selecting a modulating compound that inhibits or activates protein-protein
                                                                                                               Human adipocyte Selected Interacting Domain (SID) prey protein #1173.
                                                                                                                                      Adipocyte; protein-protein interaction; protein complex; bait-prey complex; Selected Interacting Domain; SID; drug drug discovery; metabolic disease; obseity; lipodystrophy; diabetes mellitus; type 2; non-insulin dependent; NIDDM; adipogenesis modulation; gene therapy; human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 6; SEQ ID NO 1173; 232pp; English.
                                  ADD27716 standard; protein; 368 AA.
                                                                                                                                                                                                                                                                                                                                               (HYBR-) HYBRIGENICS. (LYNX-) LYNX THERAPEUTICS INC.
                                                                                                                                                                                                                                                                                             03-MAY-2002; 2002WO-EP006333.
                                                                                                                                                                                                                                                                                                                        04-MAY-2001; 2001US-0288885P.
                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2003-111975/10.
                                                                                                                                                                                                                                                                                                                                                                                                                           N-PSDB; ADD27715
                                                                                                                                                                                                                                           WO200290544-A2.
                                                                                                                                                                                                                   Homo sapiens.
                                                                                       15-JAN-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           interactions
                                                                                                                                                                                                                                                                      14-NOV-2002
                                                                                                                                                                                                                                                                                                                                                                                       Legrain P,
                                                              ADD27716;
                                                            ö
invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Otsuki T, Wakamatsu A, Sato H, Ishii S;
Hio Y, Otsuka K, Nagai K, Irie R, Tamechika I;
Otsuka M, Nagahari K, Masuho Y;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New polynucleotides encoding full-length polypeptides, e.g. secretory and/or membrane proteins, useful for developing medicines for diseases in which the gene is involved, or as target molecules for gene therapy.
                                                                                                                                                                                                                                                                                                                        Cytostatic; Anti-inflammatory; Osteopathic; Neuroprotective; Nootropic; Gene Therapy; human; secretory protein; membrane proteins; cancer; inflammatory disease; osteoporosis; neurological disease.
                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present invention relates to novel human secretory or membrane proteins (ADA54072-ADA55710) and their coding sequences (ADA52433-ADA54071). The coding sequences are useful in the gene therapy of diseases caused by abnormalities of the proteins, e.g. cancer, inflammatory diseases, osteoporosis or neurological disease.
                                                                                                            ..
                                                                             Score 35; DB 6; Length 95;
Pred. No. 1.8e+02;
1; Mismatches 0; Indels
                                                                    92.1%; Sco...
83.3%; Pred. No. 1...
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 14; SEQ ID NO 3057; 205pp; English.
                                                                                                                                                                                                                      ADA55489 standard; protein; 310 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (HELI-) HELIX RES INST.
(REAS-) RES ASSOC BIOTECHNOLOGY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      21-MAR-2002; 2002EP-00006586.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               14-SEP-2001; 2001JP-00328381.
24-JAN-2002; 2002US-0350435P.
                                                                                                                                                                                                                                                                                                 Human protein, SEQ ID 3057.
                                                                                                                                                                                                                                                                         (first entry)
                                                              Query Match
Best Local Similarity 83.37
S; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Isogai T, Sugiyama T,
Yamamoto J, Isono Y,
Seki N, Yoshikawa T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2003-395539/38.
                                                                                                                                                       62 CVPVTC 67
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                                                                                                                             1 CVPLTC
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                                                      Ä
                                                    Sequence 95
                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                      EP1293569-A2
                                                                                                                                                                                                                                                                        20-NOV-2003
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                                                                                                                                                                                                                                               ADA55489;
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Khrebtukova I,

Мао Ј,

Whiteside S,

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The invention relates to a bait-prey complex between two adipocyte polypeptides, or between two polynucleotides encoding adipocyte polypeptides. The livention also relates to Selected Interacting Domain (SID) polypeptides which interact with selected bait polypeptides; comprising an adipocyte polynucleotide encoding SID polypeptides; vectors comprising SID polynucleotide or a SID-encoding vector; a method of selecting for a compound which modulates interactions between adipocyte polypeptides; adipocyte modulator compounds identified using the method; a plarmaceutical composition comprising an adipocyte modulator, or a SID-encoding vector or monounds identified using the method; a plarmaceutical composition comprising an adipocyte modulator or a SID-encoding vector or host cell; and a protein chip comprising adipocyte bait polypeptides. The bait-prey complexes of the invention are useful for selecting a compound that inhibits or a civiates protein-protein interactions between adipocyte polypeptides. The modulatory compounds identified can be used in the treatment of metabolic diseases such as obesity, lipodystrophy and type 2 diabetes mellitus, and in the modulation of adipogenesis. The present sequence represents a specifically claimed adipocyte SID prey polypeptide of the invention.
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Pred. No. 6.2e+02;
1; Mismatches 0; Indels
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Job time: 21.697 secs
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83.3%; Fil.
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Gaps

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Length 310;

Score 35; DB 6; Length 310. Pred. No. 5.3e+02;

92.1%; Scor. 83.3%; Pred. No. 5... 1; Mismatches

5; Conservative

Best Local Similarity

Query Match

Sequence 310 AA;

CLPLTC 267

262

1 CVPLTC 6

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5, 2004, 10:00:15; Search time 16.8485 Seconds (without alignments) 112.199 Million cell updates/sec
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| cgn2_6/prodata/2/pubpaa/US07_PUBCOMB.pep:*
| cgn2_6/prodata/2/pubpaa/RCT_NEW_PUB.pep:*
| cgn2_6/prodata/2/pubpaa/US06_NEW_PUB.pep:*
| cgn2_6/prodata/2/pubpaa/US06_PUBCOMB.pep:*
| cgn2_6/prodata/2/pubpaa/US07_NEW_PUB.pep:*
| cgn2_6/prodata/2/pubpaa/US07_NEW_PUB.pep:*
| cgn2_6/prodata/2/pubpaa/US08_NEW_PUB.pep:*
| cgn2_6/prodata/2/pubpaa/US08_PUBCOMB.pep:*
| cgn2_6/prodata/2/pubpaa/US108_PUBCOMB.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1298764 seqs, 315065143 residues
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                              US-09-761-636A-12
38
1 CVPLTC 6
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Maximum DB seq length: 200000000
                                                                                                                                                                                             September
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                                                                                                                                                                                                                                                                                                              Title:
Perfect score:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description		Semience 12, Appl	Semience 104335,	Comission of Annal	Segmence 3, Appil	Segmence 2, Appli	Segmente 1/, Appr	Somiones 2200, Ap	Sequence 46, Appl	Sequence 45, Appl	Sequence 198429,	Sequence 305/, Ap	Sequence 25, Appl	D (Sequence 272858,	seduence 3842, Ap
SUMMARIES	ID	US-09-761-6362-10	US-10-424-599-164353	US-09-826-734-122	US-09-799-514-9	US-10-016-248-2	US-10-016-248-47	US-10-408-765A-2286	US-10-016-248-46	115-10-016-248	US-10-424-599-198429	IIS-10-094-749-3057	IIS-09-983-025-25	118-10-295-023	IIS-10-424-E00-2220E0	US-10-104-047-3842	7.00
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	Query Match	100.0	100.0	94.7	94.7	94.7	94.7	94.7	94.7	94,7	92.1	92.1	92.1	92.1	89.5	89.5	
	Score	38	38	36	36	36	36	36	36	36	35	35	35	35	34	34	
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US	US-10-424-59	US-10-424-599-1	US-10-424-599-	US-10-424-599-14531	US-10-424-599-	US-10-425-114-	US-10-282-122A-	US-10-425-114-50640	US-10-425-114-5078	9	2-839-	583-10	10-262-839-	-437-963-20	739-254-R3	415		-10-054-988-8	-10-055-098-8	-10-4	-10-424-5	8-10-424-59	US-09-864-761-46679	US-10-424-599-162389	-698-6300	-466-164-65	-161-2	10-292-798-16E	09-898-570-18	3-09-839-446-
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52	58	9	62	69	103	149	158	162	187	556	1575	1587	1587	34	49	4 4		t,	4.9	55	57	117	125	164	235	256	289	289	344	344
86.8	86.8	86.8	86.8	86.8	86.8	86.8	86.8	86.8	86.8	86.8	86.8	86.8	86.8	84.2	84.2	84.2	0.4	7 .	2.40	84.2	84.2	84.2	84.2	4	84.2	4	4	**	84.2	84.2
33	e 6	33	33	33	33	33	33	33	33	33	33	33	33	32	32	32	3.3	9 6	70	32	32	32	32	32	32	32	32	32	32	32
16	17	87	19	20	21	22	23	24	25	56	27	28	29	30	31	32	33) (# L	35	36	3.7	33	39	40	41	42	43	44	45

ALIGNMENTS

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RESULT 1
US-09-761-636A-12
Sequence 12, Application US/09761636A
Sequence 12, Application US/09761636A
Sequence 12, Application US/09761636A
GENERAL INFORMATION:
APPLICANT: STACKER, Steven
APPLICANT: CRUNCAN, AMEGA
TITLE OF INVENTION: VEGF-D/VEGF-C/VEGF PEPTIDOMIMETIC INHIBITOR
FILE REPREMENTS: 1064/48505 Achen et al
CURRENT APPLICATION NUMBER: US/09/761,636A
FILE OF INVENTION: VEGF-D/VEGF-C/VEGF PEPTIDOMIMETIC INHIBITOR
CURRENT APPLICATION NUMBER: US 60/176,293
PRIOR FILING DATE: 2000-01-18
PRIOR PRILING DATE: 2000-05-16
NUMBER OF SEQ ID NOS: 34
SOFTWARE: Patentin version 3.0
I TYPE: PRT
I ORGANISM: Homo sapiens
US-09-761-636A-12

Query Match
Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps
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; Sequence 164353, Application US/10424599 ; Publication No. US20040031072A1

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GRENEAL INFORMATION:
FILE REPERBENCE: 21402-218
CURRENT FILING DATE: 2002-09-20
CURRENT FILING DATE: 2002-09-20
FRIOR PAPLICATION NUMBER: 60/294,329
FRIOR PAPLICATION NUMBER: 60/291,037
FRIOR PAPLICATION NUMBER: 60/291,037
FRIOR APPLICATION NUMBER: 60/291,037
FRIOR APPLICATION NUMBER: 60/295,648
FRIOR APPLICATION NUMBER: 60/295,173
FRIOR APPLICATION NUMBER: 60/309,258
FRIOR PAPLICATION NUMBER: 60/309,258
FRIOR PAPLICATION NUMBER: 60/309,258
FRIOR PAPLICATION NUMBER: 60/309,268
FRIOR PAPLICATION NUMBER: 60/309,268
FRIOR PAPLICATION NUMBER: 60/309,268
FRIOR APPLICATION NUMBER: 60/309,268
FRIOR FILING DATE: 2001-07-01
FRIOR FILING DATE: 2001-06-08
FRIOR FILING DATE: 2001-06-09
FRIOR FILING DATE: 2001-10-01
FRIOR APPLICATION NUMBER: 60/315,639
FRIOR APPLICATION NUMBER: 60/315,639
FRIOR FILING DATE: 2001-10-01
FRIOR APPLICATION NUMBER: 60/315,639
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TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same FILE REFERENCE: 21402-218
CURRENT APPLICATION NUMBER: US/10/016,248
CURRENT FILING DATOR NUMBER: 60/254,329
PRIOR APPLICATION NUMBER: 60/254,329
                                                                                                                                                                                                                                                                       Score 36; DB 9; Length 613;
Pred. No. 3e+02;
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Best Local Similarity 83.3%; Pred. No. 1.4e+03;
Matches 5; Conservative 1; Mismatches 0;
                                                                                                                                                                                                                                                                                                                       1; Mismatches
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, Publication No. US20040033491A1
                                                                                                                                                                                                                                                                              94.7%;
                                                                 1999-09-03
                        2000-08-29
                                                                                                                   PatentIn Ver. 2.0
PRIOR APPLICATION NUMBER: E PRIOR FILING DATE: 2000-08-9PIOR RELING DATE: 1999-09-NUMBER OF SEQ ID NOS: 19-SOFTWARE: Patentin Ver: 2.0
                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 83.3
Matches 5; Conservative
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2486 CVPITC 2491
                                                                                                                                                                                                               ORGANISM: Homo sapiens
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                                                                                                                                         SEQ ID NO 9
LENGTH: 613
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-10-016-248-2
                                                                                                                                                                                                                                       US-09-799-514-9
                                                                                                                                                                                          TYPE: PRT
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TITLE OF INVENTION: Immunoglobulin Superfamily Polynucleotides, Polypeptides, and Ar
TITLE REPERBUCE: P7015F1
CURRENT APPLICATION NUMBER: US/09/799,514
CURRENT FILING DATE: 2001-03-07
                                 APPLICANT: La Rosa Thomas J
APPLICANT: A Rosa Thua
APPLICANT: Cao Yongwai
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REPERENCE: 38-21 (53223) B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
SEQ ID NOS: 285684
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Pred. No. 96;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 45;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                    ; OTHER INFORMATION: Clone ID: PAT_MRT3847_119429C.1.pep
US-10-424-599-164353
                                                                                                                                                                                                                                                                                                                                                                                                                                                          12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.0%; Score 38; DB 100.0%; Pred. No. 12;
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1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Mismatches
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 122
LENGTH: 175
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; Sequence 9, Application US/09799514
; Patent No. US20020065220A1
; GENERAL INPORMATION:
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83.3%;
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Best Local Similarity 100.
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Matches 5; Conservative
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US-09-826-734-122
                                                                                                                                                                                                                                                                                                                                               ORGANISM: Glycine max
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US-09-826-734-122
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Score 36; DB 12; Length 3508;
Pred. No. 1.5e+03;
1; Mismatches 0; Indels (
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                                               PRIOR APPLICATION NUMBER: 60/254,329
PRIOR FILING DATE: 2000-12-08
PRIOR FILING DATE: 2000-12-08
PRIOR FILING DATE: 2001-05-15
PRIOR FILING DATE: 2001-05-15
PRIOR FILING DATE: 2000-05-15
PRIOR APPLICATION NUMBER: 60/25,648
PRIOR PILING DATE: 2000-06-08
PRIOR PILING DATE: 2001-06-08
PRIOR PILING DATE: 2001-06-08
PRIOR PILING DATE: 2001-07-31
PRIOR PILING DATE: 2001-08-29
NUMBER OF SEQ ID NOS: 167
SOFTWARE: PALENTING VARBER: 60/315,639
NUMBER: PALENTING DATE: 2001-08-29
NUMBER: PALENTING DATE: 2001-08-29
NUMBER: PALENTING DATE: 2001-08-29
NUMBER: PALENTING DATE: 2001-08-29
NUMBER: PALENTING VARBER: 60/315,639
PRIOR PILING DATE: 2001-08-29
NUMBER: PALENTING VARBER: 60/315,639
PRIOR PILING DATE: 2001-08-29
NUMBER: PALENTING VARBER: PALENTING VET: 2.1
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Publication No. US20040033491A1
GENERAL INFORMATION:
                                  2002-09-20
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Best Local Similarity 83.3
Matches 5; Conservative
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CRGANISM: Mus musculus
US-10-016-248-45
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                            CURRENT
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| Publication No. US20040101874A1
| GENERAL INFORMATION:
| APPLICANT Ghosh, Soumitra S. |
| APPLICANT: Fally, Edun D. |
| APPLICANT: Fally, Edun D. |
| APPLICANT: Glosn, Bradford W. |
| APPLICANT: Glosn, 
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US-10-016-248-46
; Sequence 46, Application US/10016248
; Publication No. US20040033491A1
; Publication No. US20040033491A1
; APPLICANT: Alsobrook et al.
; TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same; FILE REFERENCE: 21402-218
; CURRENT APPLICATION NUMBER: US/10/016,248
PRIOR FILING DATE: 2000-12-08
PRIOR APPLICATION NUMBER: 60/291,037
PRIOR FILING DATE: 2010-16-15
PRIOR FILING DATE: 2010-16-15
PRIOR FILING DATE: 2001-12-18
PRIOR PILING DATE: 2001-12-14
PRIOR PILING DATE: 2001-06-08
PRIOR PILING DATE: 2001-06-18
PRIOR PILING DATE: 2001-06-18
PRIOR PILING DATE: 2001-07-31
PRIOR PILING DATE: 2001-07-31
PRIOR PILING DATE: 2001-07-31
PRIOR PILING DATE: 2001-01-10
PRIOR PILING DATE: 2001-10-11
PRIOR PILING DATE: 2001-08-29
NUMBER OF SEQ ID NOS: 167
SEQ ID NO 47
LENGTH: 3389
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Best Local Similarity 83.3.
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Best Local Similarity 83.3
Matches 5; Conservative
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ORGANISM: Homo sapiens
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2677 CVPITC 2682
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LENGTH: 3389
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RESULT 12
US-09-883-025-25
i Sequence 25, Application US/09983025
j Fublication No. US20030124529A1
general information:
   APPLICANT: OVERGARD, Michael T.
   TITLE OF INVENTION: PREGNANCY-ASSOCIATED PLASMA PROTEIN-A2
   TITLE OF INVENTION: PREGNANCY-ASSOCIATED PLASMA PROTEIN-A2
   TITLE OF INVENTION: PREGNANCY-ASSOCIATED PLASMA PROTEIN-A2
   CURRENT APPLICATION NUMBER: US 60/241,840
   PRIOR FILING DATE: 2000-10-20
   PRIOR FILING DATE: 2000-10-20
   PRIOR FILING DATE: 2000-10-20
   PRIOR FILING DATE: 2000-10-20
   NUMBER OF SEQ ID NOS: 25
   SOFTWARE: Patentin version 3.1
   SEQ. 10 NO 5.55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Murray, Richard
APPLICANT: Watson, Susan R.
APPLICANT: Ess Biotechnology, Inc.
TITLE OF INVENTION: Methods of Diagnosis of Cancer, Compositions and
TITLE OF INVENTION: Methods of Screening for Modulators of Cancer
FILE REFERENCE: 018501-012500US
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92.1%; Score 35; DB 10; Length 1627;
Best Local Similarity 83.3%; Pred. No. 1.1e+03;
Matches 5; Conservative 1; Mismatches 0; Indels
                                        Score 35; DB 15; Length 31
Pred. No. 2.4e+02;
1; Mismatches 0; Indels
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PRIOR PILING DATE: 2000-09-15
PRIOR PILING DATE: 2000-15-15
PRIOR PILING DATE: 2001-11-13
PRIOR APPLICATION NUMBER: US 60/335,394
PRIOR PILING DATE: 2001-11-15
PRIOR PILING DATE: 2001-11-15
PRIOR APPLICATION NUMBER: US 60/332,464
PRIOR PILING DATE: 2001-11-21
PRIOR APPLICATION NUMBER: US 60/334,393
PRIOR FILING DATE: 2001-11-29
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Publication No. US20030232350A1

GENERAL INFORMATION:
APPLICANT: Afar, Daniel
APPLICANT: Ginsberg, Wendy M.
APPLICANT: Ginsberg, Wendy M.
APPLICANT: Gish, Kurt C.
APPLICANT: Glynne, Richard
APPLICANT: Hevezi, Peter A.
APPLICANT: Hevezi, Peter A.
                                                                                             Conservative
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, ORGANISM: Homo sapiens
US-09-983-025-25
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262 CLPLTC 267
                                             Ouery Match
Best Local Similarity
Matches 5; Conserv
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US-10-094-749-3057
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APPLICANT:
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                                   Sequence 198429, Application US/10424599
Publication No. US20040031072A1
GENERAL INFORMATION:
APPLICANT: La Rosa Thomas J
APPLICANT: Zhou Yihua
APPLICANT: Zhou Yihua
APPLICANT: Zhou Yihua
APPLICANT: Alou Yihua
APPLICANT: Alou Yihua
APPLICANT: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(5323)B
CURRENT APPLICANION NUMBER: US/10/424,599
CURRENT PLING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NOS: 285684
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        , OTHER INFORMATION: Clone ID: PAT_MRT3847_21205C.1.pep
US-10-424-599-198429
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LOCATION: (1)..(127)
OTHER INFORMATION: unsure at all Xaa locations
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: NAGAHARI, KENJI
APPLICANT: NAGAHARI, KENJI
ALITLE OF INVENTION: NOVEL FULL-LENGTH CDNA
FILE REPERENCE: 084335/0160
CURRENT APPLICATION NUMBER: US/10/094,749
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT FILING DATE: 2002-03-12
PRIOR APPLICATION NUMBER: 60/350,435
PRIOR FILING DATE: 2002-01-24
PRIOR APPLICATION NUMBER: JP 2001-328381
NUMBER: APPLICATION NUMBER: JP 2001-328381
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Publication No. US20030219741A1
GENERAL INFORMATION:
APPLICANT: ISOGAI, TAKAO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SUGIYAMA, TAKAO
SUGIYAMA, TOMOYASU
OTSUKI, TERSUI
WAKAMATSU, AI
SATO, HIROYUKI
ISHII, SHIZUKO
YAMAMOTO, JUN-ICHI
ISONO, YUUKO
HIO, YUKI
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OTSUKA, MOTOYUKI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TAMECHIKA, ICHIRO SEKI, NAOHIKO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OTSUKA, KAORU
NAGAI, KEIICHI
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SOFTWARE: Patentin Ver. 2
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ORGANISM: Homo sapiens
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ORGANISM: Glycine max
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                                     US-10-424-599-198429
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APPLICANT:
APPLICANT:
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Gaps

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SOFTWARE: Patentin Ver. 2.1
                                               SEQ ID NO 3842
LENGTH: 570
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Sequence 272858, Application US/10424599
Publication No. US20040031072A1
GENERAL INFORMATION:
APPLICANT: La Rosa Thomas J
APPLICANT: La Rosa Thomas J
APPLICANT: Zhou Yihua
APPLICANT: Zhou Yihua
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(5)223)8
CURRENT FILING DATE: 2003-04-28
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 272858
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PRIOR APPLICATION NUMBER: US 60/340,376
PRIOR FILING DATE: 2001-12-14
PRIOR APPLICATION NUMBER: US 60/347,211
PRIOR FILING DATE: 2002-01-08
PRIOR FILING DATE: 2002-01-10
PRIOR FILING DATE: 2002-01-10
PRIOR PLING DATE: 2002-02-08
PRIOR APPLICATION NUMBER: US 60/355,250
PRIOR PLING DATE: 2002-02-08
PRIOR FILING DATE: 2002-02-03
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Pred. No. 1.1e+03;
1; Mismatches 0; Indels (
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Publication No. US20030236392A1
GENERAL INFORMATION:
APPLICANT: HELIX RESEARCH INSTITUTE
APPLICANT: HELIX RESEARCH INSTITUTE
TILLE OF INVENTION: No. US20030236392A1e1 full length cDNA
FILE REFERENCE: H1-A010S
CURRENT APPLICATION NUMBER: US/10/104,047
CURRENT FILING DATE:
PRIOR APPLICATION NUMBER:
PRIOR FILING DATE:
NUMBER OF SEQ ID NOS: 4096
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    92.1%;
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Best Local Similarity 83.3
Matches 5; Conservative
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Best Local Similarity 83.3
Matches 5, Conservative
                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT
ORGANISM: Homo sapiens
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1410 CVPVTC 1415
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ORGANISM: Glycine max
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US-10-424-599-272858
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US-10-295-027-663
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LENGTH: 162
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; SEQ ID NO 3842
; INCOMES 570
; TYPE: BRT
; ORGANISM: Homo sapiens
US-10-104-047-3842
Query Match
Best Local Similarity 83.3%; Pred. No. 6.4e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps
QY 1 CVPLTC 6
Db 186 CVPLSC 191
Search Completed: September 5, 2004, 10:29:22
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* 3000 K Street, N.W. Washington, D.C.
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COMPUTER READABLE FORM:
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CITY: Wa
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Sequence 3, Appli
Patent No. 5208144
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Patent No. 5208144
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Sequence 2, Appli
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                                                       5, 2004, 09:55:30 ; Search time 5.33333 Seconds
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58.079 Million cell updates/sec
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(Ggn2_6/ptodata/2/iaa/5A_COMB.pep:*

(Ggn2_6/ptodata/2/iaa/5B_COMB.pep:*

(Ggn2_6/ptodata/2/iaa/6A_COMB.pep:*

(Ggn2_6/ptodata/2/iaa/6B_COMB.pep:*

(Ggn2_6/ptodata/2/iaa/PcTUS_COMB.pep:*

(Ggn2_6/ptodata/2/iaa/pcTuS_COMB.pep:*
GenCore version 5.1.6
(c) 1993 - 2004 Compugen Ltd.
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US-08-325-071-61

US-08-325-071-65

US-08-461-004A-65

US-08-325-071-56

US-08-325-071-67

US-08-325-071-67

US-08-325-071-67

US-08-461-004A-59

US-08-461-004A-59

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US-08-461-004A-63

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US-08-461-004A-63

US-09-361-709B-3

S208144-37

US-09-561-709B-1

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                                                                                                                                                                           Total number of hits satisfying chosen parameters:
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US-08-652-877-86
US-08-652-877-88
US-08-652-877-88
                                                                                                                                                             389414 seqs, 51625971 residues
                                  OM protein - protein search, using sw model
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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38
                                                                                                                                                                                                 seq length: 0
seq length: 200000000
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Match Length
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Perfect score:
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Maximum DB
                                                                                                               Sequence:
                                                                                                                                                             Searched:
                                                     Run on:
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GENERAL INFORMATION:
APPLICANT: Gary L. Breton et al.
APPLICANT: Gary L. Breton et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
TITLE OF INVENTION: BAUMANII FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: GTC99-03PA
CURRENT APPLICATION NUMBER: US/09/328,352
CURRENT FILING DATE: 1999-06-04
NUMBER OF SEQ ID NOS: 8252
SEQ ID NO 4708
LENGTH: 159
                                              Sequence 5, Appli
Sequence 17751, A
Sequence 32545, A
Sequence 34, Appl
Sequence 24, Appl
Sequence 28, Appl
Sequence 1, Appli
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   Sequence 9, #
Sequence 5, #
Sequence 5, #
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Pred. No. 1.2e+02;
0; Mismatches 1; Indels
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APPLICANT: COBON, Stewart Gary
APPLICANT: MOORE, Joana Terry
APPLICANT: MOORE, Joana Terry
APPLICANT: WILLADSEN, Law Anthony York
APPLICANT: WILLADSEN, Peter
APPLICANT: REMP, David Harold
APPLICANT: RIDING, George Affred
APPLICANT: RIDING, George Affred
APPLICANT: RIDING, Reith No. 5587311man
TITLE OF INVENTION: DNA Encoding A Cell Membrane
TITLE OF INVENTION: Glycoprotein Of A Tick Gut
NUMBER OP SEQUENCES: 71
CORRESPONDENCE ADDRESS:
           US-08-0318-13-5
US-08-0318-13-5
US-08-356-832-5
US-09-252-991A-17751
US-09-252-991A-18787
US-09-252-991A-34
US-09-055-699-34
US-09-055-699-34
US-09-661-468-34
US-09-661-468-34
US-09-676-165-34
US-09-976-165-34
                                                                                                                                                                                                                                                        US-08-033-873-8
US-08-033-873-15
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Patent No. 6562958
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Patent No. 5587311
GENERAL INFORMATION:
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ORGANISM: Acinetobacter baumannii
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   86.8%;
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Best Local Similarity
Matches 5; Conserv
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881.6
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Length 549;
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                                                                                                                                     OPERATING SYSTEM: PC-DOS/MS-UOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/461,004A
FILING DATE: 04-JUN-1995
FRIOR APPLICATION NUMBER: US 08/325,071
FILING DATE: 19-OCT-1994
APPLICATION NUMBER: US 08/062,109
FRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/926,368
FILING DATE: 17-MAY-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/926,368
FILING DATE: 07-JUL-1988
FILING DATE: 06-JUL-1988
FILING DATE: 06-JUL-1988
FILING DATE: 27-NOV-1987
FILING DATE: 10-OCT-1997
FILING DATE: 10-OCT-1997
FILING DATE: 10-JUN-1987
FILING DATE: 27-NOV-1986
ATCORNEY/AGENT INFORMATION:
REFERENCE/AGENT INFORMATION:
NAME: REFERENCE/DOCKET NUMBER: 60042/152
FELEFRAX: 202 672 5399
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APPLICANT: SRISKANTHA, Alagacone
APPLICANT: RIDING, George Alfrach
APPLICANT: RAND, Keith No. 5587311man
ITILE OF INVENTION: DNA Encoding A Cell Membrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          86.8%; Score 33; DB 3; I
83.3%; Pred. No. 3.7e+02;
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MOORE, Joanna Terry
JOHNSON, Law Anthony York
WILLADSEN, Peter
                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 65, Application US/08325071
Patent No. 5587311
GENERAL INFORMATION:
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INFORMATION FOR SEQ ID NO: 61:
SEQUENCE CHARACTERISTICS:
LENGTH: 549 amino acids
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amino acid
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Matches 5, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            66 CVPTTC 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 CVPLTC 6
                      20007-5109
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APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-08-461-004A-61
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APPLICANT:
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APPLICANT:
COUNTRY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
APPLICANT: COBON, Stewart Gary
APPLICANT: COBON, Stewart Gary
APPLICANT: MOORE, Joanna Terry
APPLICANT: WILLADSEN, Law Anthony York
APPLICANT: WILLADSEN, Peter
APPLICANT: SRISKANTHA, Alagacone
APPLICANT: RIDING, George Alfred
APPLICANT: RIDING, George Alfred
APPLICANT: RAND, Keith No. 6235283man
TITLE OF INVENTION: Glycoprotein Of A Tick Gut
NUMBER OF SEQUENCES: 71
                      COMPUTER: IEM PC compatible
COMPUTER: IEM PC compatible
COMPUTER: IEM PC compatible
SOUTHARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/325,071
FILING DATE: 14-0-0-1993
PRIOR APPLICATION NUMBER: US 08/062,109
FILING DATE: 17-MAY-1993
PRIOR APPLICATION NUMBER: US 07/926,368
FILING DATA:
APPLICATION NUMBER: US 07/926,368
FILING DATA:
APPLICATION NUMBER: US 07/926,368
FILING DATA:
APPLICATION NUMBER: O7/22,196
FILING DATA: COMPANIER: US 07/926,368
FILING DATA: TOWN-1992
PRILING DATA: APPLICATION NUMBER: DCT/AU87/00401
FILING DATA: APPLICATION DATA:
APPLICATION NUMBER: AU P12570
FILING DATA: 16-0-0-1987
FILING DATA: 16-0-0-1987
FRILNG DATA: 16-0-0-1987
FRILNG DATA: 16-0-0-1987
FRILNG DATA: 16-0-0-1987
FRILNG DATA: APPLICATION DATA: APPLICATION NUMBER: AU P12570
FILING DATA: APPLICATION NUMBER: AU P1956
FILING DATA: APPLICATION NUMBER: AU P1996
FILING DATA: APPLICATION NUMBER: AU P1999996
FILING DATA: APPLICATION NUMBER: AU P1996
FILING DATA: APPLICATION NUMBER: AU P1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPRAX: 202 672 5300
TELEPRAX: 202 672 5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 61:
SEQUENCE CHARACTERISTICS:
LENGTH: 549 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 61, Application US/08461004A Patent No. 6235283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEE: Foley & Lardner: 3000 K Street, N.W. Washington, D.C.
     MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 83.3
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CVPTTC 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 CVPLTC 6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-08-325-071-61
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CITY: Wa
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Gaps

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86.8%; Score 33; DB 3; Length 620;
83.3%; Pred. No. 4.2e+02;
iive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/461,004A
FILING DATE: 04-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/325,071
FILING DATE: 10-OCC-1994
FILING DATE: 10-OCC-1994
PRIOR APPLICATION NUMBER: US 08/062,109
FILING DATE: 17-MAY-1993
PRIOR APPLICATION NUMBER: US 07/926,368
FILING DATE: 07-AUG-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/242,196
FILING DATE: 06-JUL-1988
FILING DATE: 06-JUL-1988
FILING DATE: 06-JUL-1988
FILING DATE: 06-JUL-1988
FILING DATE: 07-VUL-1988
     APPLICANT: RIDING, George Alfred
APPLICANT: RAND, Keith No. 6235283man
TITLE OF INVENTION: DNA Encoding A Cell Membrane
TITLE OF INVENTION: Glycoprotein Of A Tick Gut
NUMBER OF SEQUENCES: 71
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                60042/152
                                                                                                                                                                                                                                                                                  ZIP: 20007-5109
COMPUTER REALABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RILING DATE: 19-JUN-1987

PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: 40 PH9196

PILING DATE: 27-NOV-1986

ATTORNEY/AGENT INFORMATION:
NAME: BENT, SEEPHEN A:
REGISTRATION NUMBER: 60042/1
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFHONE: 202 672 5300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; Sequence 56, Application US/08325071; Patent No. 5587311; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
APPLICATION NUMBER: AU PI4912
FILING DATE: 16-OCT-1987
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AU PI2570
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             620 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEX: 904136
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                   CITY: Washington, D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity 83.3
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; MOLECULE TYPE: protein US-08-461-004A-65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           amino acid
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US-08-325-071-56
                                                                                                                                                                                                                                                              COUNTRY:
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                                                                                                                                                                                                                                                                                                                      CURENTIANG SYSTEM: WC-UCUS/MS-DUS
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/325,071
FILING DATE: US/08/325,071
FILING DATE: US/08/33
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/062,109
FILING DATE: 17-MAY-1993
PRIOR APPLICATION NUMBER: US 07/926,368
FILING DATE: 07-AUG-1992
PRIOR APPLICATION NUMBER: US 07/926,368
FILING DATE: 07-AUG-1992
PRIOR APPLICATION NUMBER: PCT/AUB7/00401
FILING DATE: 10-AUC-1988
PRIOR APPLICATION NUMBER: AU P14912
FILING DATE: 12-AU0-1987
PRIOR APPLICATION NUMBER: AU P14912
FILING DATE: 15-AUN-1987
PRIOR APPLICATION NUMBER: AU P1997
FILING DATE: 15-AUN-1987
PRIOR APPLICATION DATA:
APPLICATION NUMBER: AU P1996
FILING DATE: 19-AUN-1987
PRIOR APPLICATION DATA:
APPLICATION NUMBER: AU P1996
FILING DATE: 19-AUN-1987
PRIOR APPLICATION NUMBER: AU P1996
FILING DATE: 19-AUN-1987
PRIOR APPLICATION NUMBER: AU P1996
FILING DATE: 19-AUN-1987
APPLICATION NUMBER: AU P1996
FILING DATE: 19-AUN-1987
APPLICATION NUMBER: AU P1998
FILING DATE: 19-AUN-1987
APPLICATION NUMBER: 29-768
FILING DATE: NUMBER: 29-768
TITLE OF INVENTION: Glycoprotein Of A Tick Gut
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER: 60042/111 BIAU TELECOMMUNICATION INFORMATION: TELEPHONE: 202 672 5300 TELEPAGE: 202 672 5399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COBON, Stewart Gary
MODRE, Joanna Terry
JOHNSON, Law Anthony York
WILLADSEN, Peter
KEMP, David Harold
SRISKANTHA, Alagacone
                                                                                                                               CITY: Washington, D.C.
COUNTRY: USA
ZIP: 20077-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM ECOMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; Sequence 65, Application US/08461004A
; Patent No. 6235283
; GENERAL INFORMATION:
   APPLICANT: COBON, Stewart Gary
   APPLICANT: MOORE, Joanna Terry
   APPLICANT: JOHNSON, Law Anthony York
   APPLICANT: WILLADSEN, Peter
   APPLICANT: KEMP, David Harold
   APPLICANT: SRISKANTHA, Alagacone
                                                                               IE: Foley & Lardner 3000 K Street, N.W
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 83.3%,
Thes 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               : 620 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEX: 904136
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                       NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: FOLGY & La
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: protein US-08-325-071-65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       117 CVPTTC 122
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US-08-461-004A-65
                                                                                                             STREET:
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APPLICANT: COBON, Stewart Gary
APPLICANT: MOORE, JOANNA TERRY
APPLICANT: WILLADSEN, Law Anthony York
APPLICANT: WILLADSEN, PEter
APPLICANT: WILLADSEN, PEter
APPLICANT: REMP. David Harold
APPLICANT: REMP. George Alfred
APPLICANT: RIDING, George Alfred
APPLICANT: RAND, Keith No. 5587311man
TITLE OF INVENTION: DNA Encoding A Cell Membrane
TITLE OF INVENTION: Glycoprotein of A Tick Gut
NUMBER OF SEQUENCES: 71
CORRESPONDENCE ADDRESS:
ADDRESSEE: FOLEV F.
STRFFT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER PROPERTY STREET: 3000 K Street, N.W.
CITY: Washington, D.C.
COUNTRY: USA
ZIP: 20007-5109
COMPUTER READBALE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER READBALE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: DAW PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/325,071
FILING DATE: 14-OCT-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/062,109
FILING DATE: 17-MAY-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/926,368
FILING DATE: 07-AUG-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 05-704-196
FILING DATE: 10-404-198
REING APPLICATION DATA:
APPLICATION NUMBER: AU P14912
FILING DATE: 10-6-71-198
FILING DATE: 10-6-71-198
FILING DATE: 10-6-71-198
FILING DATE: 10-704-198
APPLICATION NUMBER: AU P19196
FILING DATE: 10-704-198
APPLICATION NUMBER: AU P19196
FILING DATE: 10-704-198
APPLICATION NUMBER: 39,768
REFERENCE/DOCKET NUMBER: 39,768
REFERENCE/DOCKET NUMBER: 59,768
REFERENCE/DOCKET NUMBER: 59,768
REFERENCE/DOCKET NUMBER: 20,768
REFERENCE/DOCKET NUMBER: 20,763
TELLEPAK: 20,2672 5399
                                                                                        Sequence 59, Application US/08325071
Patent No. 5587311
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: 202 672 5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 59
SEQUENCE CHARACTERISTICS:
LENGTH: 650 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match

86.8%; Score 33; DB 1; Length 650;
Best Local Similarity 83.3%; Pred. No. 4.4e+02;
Matches 5; Conservative 0; Mismatches 1; Indels
APPLICANT: COBON, Stewart Gary
APPLICANT: MOOSE, Joanna Terry
APPLICANT: MOOSE, Joanna Terry
APPLICANT: WILLADSEN, Law Anthony York
APPLICANT: WILLADSEN, Peter
APPLICANT: KEMP, David Harold
APPLICANT: RISKANTHA, Alagacone
APPLICANT: RIDING, George Alfred
APPLICANT: RAND, Keith No. 5587311man
TITLE OF INVENTION: DNA Encoding A Cell Membrane
TITLE OF INVENTION: Glycoprotein Of A Tick Gut
NUMBER OF SEQUENCES: 71
CORRESPONDENCES: 71
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lastner
STREET: 3000 K Street, N.W.
CUTY: Washington, D.C.
COUNTRY: USA
ZIP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY: USA

ZIP: 20007-5109

COMPUTER READBLE FORM:
MEDIUW TYPE: Floppy disk
COMPUTER READBLE FORM:
MEDIUW TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US 08/062,109
FILING DATE: U-AV-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/226,368
FILING DATE: 07-AUG-1992
PRIOR APPLICATION NUMBER: US 07/226,368
FILING DATE: 07-AUG-1992
PRIOR APPLICATION NUMBER: WO 1/242,196
FILING DATE: 10-VOV-1987
PRIOR APPLICATION NUMBER: AU P14912
FILING DATE: 10-VOV-1987
PRIOR APPLICATION NUMBER: AU P14912
FILING DATE: 10-VOV-1987
PRIOR APPLICATION NUMBER: AU P12570
FILING DATE: 10-VOV-1987
PRIOR APPLICATION NUMBER: AU P12570
FILING DATE: 10-VON-1986
FILING DATE: 19-VOV-1987
PRIOR APPLICATION NUMBER: AU P1956
FILING DATE: 19-VOV-1986
ATTORNEY/AGENT INFORMATION:
NAME: BENT; Stephen A.
REGISTRATION NUMBER: 23-NOV-1986
ATTORNEY/AGENT NUMBER: 29-NOV-1986
ATTORNEY/AGENT NUMBER: 29-NOV-1987
REGISTRATION NUMBER: 20-NOV-1987
REGISTRATION N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       60042/111 BIAU
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 202 672 5399
TELEFAX: 202 672 5399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEX: 904136
INFORMATION FOR SEQ ID NO: 56:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          : 650 amino acids
amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       linear
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0
                                                 Query Match

86.8%; Score 33; DB 1; Length 650;
Best Local Similarity 83.3%; Pred. No. 4.4e+02;
Matches 5; Conservative 0; Mismatches 1; Indels
MOLECULE TYPE: protein US-08-325-071-59
                                                                                                                                                                  147 CVPTTC 152
                                                                                                                             1 CVPLTC 6
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Gaps ; 0

147 CVPTTC 152

RESULT 7 US-08-325-071-59

1 CVPLTC 6

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COUNTRY: USA

ZIP: ZO007-1919

ZONFUTER: ERADABLE FORM:
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk

CONFUTER: IRM PC COMBATIAL

CONFUTER: PC-DOS/MS-DOS

SOFTWARE: PARTICATION DATA:
APPLICATION NUMBER: US/68/325,071

FILING DATE: 14-0CT-1993

FILING DATE: 17-MAY-1993

PRIOR APPLICATION NUMBER: US/68/326,109

FILING DATE: 17-MAY-1993

PRIOR APPLICATION NUMBER: US/68/368

FILING DATE: US/64/3196

FILING DATE: US/64/3197

FILING DATE: US/6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: RIDING, George Alfred
APPLICANT: RIDING, George Alfred
APPLICANT: RAND, Keith No. 558731man
TITLE OF INVENTION: DNA Encoding A Cell Membrane
TITLE OF INVENTION: Glycoprotein Of A Tick Gut
CORRESONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
                                                                                                                                                                                                                                GENERAL INFORMATION:
APPLICANT: COBON, Stewart Gary
APPLICANT: MOORE, Joanna Terry
APPLICANT: JOHNSON, Law Anthony York
APPLICANT: WILLANSEN, Peter
APPLICANT: KEMP, David Harold
APPLICANT: SRISKANTHA, Alagacone
                                                                                                                                                       US-08-325-071-67
; Sequence 67, Application US/08325071
; Patent No. 5587311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Foley & Lardner
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amino acid
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LENGTH: 650 amino acid
147 CVPTTC 152
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COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
SOFTWARE: Patentin Release #1.0, Version #1.25
APPLICATION NUMBER: US/08/325,071
FILING DATE: 14-OCT-1993
RIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/062,109
FILING DATE: 07-AUG-1992
RIOR APPLICATION NUMBER: US 07/226,368
FILING DATE: 07-AUG-1992
RIDING APPLICATION NUMBER: US 07/242,196
FILING DATE: 0-UL-1988
FILING DATE: 10-UNV-1987
RIDING APPLICATION NUMBER: PCT/AUB7/00401
APPLICATION NUMBER: BCT/AUB7
RIDING DATE: 16-OCT-1987
RIDING DATE: 16-OCT-1987
RIDING APPLICATION NUMBER: AU P12570
FILING DATE: 19-UNN 1987
RAPPLICATION NUMBER: AU P19196
FILING DATE: 27-NOV-1986
APPLICATION NUMBER: AU PH9196
FILING DATE: 27-NOV-1986
ATTICKED BATE: 29-768
                                                                                                                                                          APPLICANT: COBON, Stewart Gary
APPLICANT: COBON, Law Anthony York
APPLICANT: MOORE, Joanna Terry
APPLICANT: MILLADSEN, Law Anthony York
APPLICANT: KEMP, David Harold
APPLICANT: KEMP, David Harold
APPLICANT: KEMP, David Harold
APPLICANT: RIDING, George Alfred
APPLICANT: RAND, Keith No. 5587311man
TITLE OF INVENTION: DNA Encoding A Cell Membrane
TITLE OF INVENTION: Glycoprotein Of A Tick Gut
NUMBER OF SEQUENCES: 71
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             60042/111 BIAU
         RESULT 8
US-08-325-071-63
Sequence 63, Application US/08325071
Patent No. 5587311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEE: Foley & Lardner: 3000 K Street, N.W. Washington, D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER: 60
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202 672 5300
TELEFAX: 202 672 5399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEX: 904136
INFORMATION FOR SEQ ID NO: 63:
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Best Local Similarity 83.3%;
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
LENGTH: 650 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-325-071-63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STREET:
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86.8%; Score 33; DB 1; Length 650; 83.3%; Pred. No. 4.4e+02;

MOLECULE TYPE: protein US-08-325-071-67

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Gaps ..

Score 33; DB 1; Length 650; Pred. No. 4.4e+02; 0; Mismatches 1; Indels

Query Match Best Local Similarity

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Gaps
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                                                                                                                                  86.8%; Score 33; DB 3; Length 650;
83.3%; Pred. No. 4.4e+02;
tive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OFFRAILING SYSIEM:
CURRENT APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE: 04-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/325,071
FILING DATE: 19-OCT-1994
PROR APPLICATION NUMBER: US 08/062,109
FILING DATE: 17-MAX-1993
FILING DATE: 17-MAX-1993
FILING DATE: 07-MAX-1993
FILING DATE: 07-MAX-1993
FILING DATE: 07-MAX-1993
FILING DATE: 07-MAX-1992
FILING DATE: 07-MAX-1992
FILING DATE: 10-MABER: US 07/242,196
FILING DATE: 10-MABER: US 07/242,196
FILING DATE: 10-MABER: DCT/AU87/00401
FILING DATE: 17-MAX-1993
FILING DATE: 16-MAX-1993
FILING DATE: 16-MAX-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: COBON, Stewart Gary
APPLICANT: MOORE, Joanna Terry
APPLICANT: MOORE, Joanna Terry
APPLICANT: MILLADSEN, Law Anthony York
APPLICANT: WILLADSEN, David Harold
APPLICANT: KEMP, David Harold
APPLICANT: RIBING, George Alfred
APPLICANT: RIBING, George Alfred
APPLICANT: RIDING, George Alfred
APPLICANT: RAND, Keith No. 6235283man
TITLE OF INVENTION: DNA Encoding A Cell Membrane
TITLE OF INVENTION: Glycoprotein Of A Tick Gut
NUMBER OF SEQUENCES: 71
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardnor-
STREET: 3000 W ^ CLATANGORNORY
CITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     60042/152
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COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA:
APPLICATION NUMBER: AU P12570
FILING DATE: 19-UN-1987
PRIOR APPLICATION DATA:
APPLICATION NUMBER: AU PH9196
FILING DATE: 27-NOV-1986
ATTORNEY/AGENT INFORMATION:
NAME: BENT, SCEPHON A.
REGISTRATION NUMBER: 29,768
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE/DOCKET NUMBER: 60
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202 672 5300
                                                                                                                  Query Match
Best Local Similarity 83.3'
                           , MOLECULE TYPE: protein US-08-461-004A-56
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                               147 CVPTTC 152
                                                                                                                                                                                                                                                                                                    1 CVPLTC 6
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US-08-461-004A-59
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       Gaps
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CULTI: WASAILINGTON, D.C.
CULTI: WASAILINGTON, D.C.
ZIP: 20007-5109
COMPUTER READBALE FORM:
MEDIUW TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN RC-BOS/MS-DOS
SOFTWARE: PATENTIN NUMBER: US/08/461,004A
FILING DATE: 04-JUN-1995
RRIOR APPLICATION NUMBER: US 08/325,071
FILING DATE: 19-OCT-1994
PRIOR APPLICATION NUMBER: US 07/926,368
FILING DATE: 07-MG-1992
PRIOR APPLICATION NUMBER: US 07/926,368
FILING DATE: 07-MG-1992
PRIOR APPLICATION NUMBER: US 07/926,368
FILING DATE: 10-WG-1992
PRIOR APPLICATION NUMBER: US 07/926,368
FILING DATE: 10-WG-1992
PRIOR APPLICATION NUMBER: US 07/926,368
FILING DATE: 10-WG-1993
PRIOR APPLICATION NUMBER: US 07/926,368
FILING DATE: 10-WG-1993
PRIOR APPLICATION NUMBER: AU P1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: AU P1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: AU P19570
FILING DATE: 10-WG-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: AU P1996
FILING DATE: 17-WG-1986
ATTORNEY/AGENT INFORMATION:
NAME: BENT: Stephen A:
RESISTRATION NUMBER: 20-MG-1987
RESISTRATION NUMBER: 20-MG-1986
ATTORNEY/AGENT INFORMATION:
NAME: RESISTRATION NUMBER: 20-MG-10-MG-10-MG-10-MG-10-MG-10-MG-10-MG-10-MG-10-MG-10-MG-10-MG-10-MG-10-MG-10-MG-10-MG-10-MG-10-MG-10-MG-10-MG-10-MG-10-MG-10-MG-10-MG-10-MG-10-MG-10-MG-10-MG-10-MG-10-MG-10-MG-10-MG-10-MG-10-MG-10-MG-10-MG-10-MG-10-MG-10-MG-10-MG-10-MG-10-MG-10-MG-10-MG-10-MG-10-MG-10-MG-10-MG-10-MG-10-MG-10-MG-10-MG-10-MG-10-MG-10-MG-10-MG-10-MG-10-MG-10-MG-10-MG-10-MG-10-MG-10-MG-10-MG-10-MG-10-MG-10-MG-10-MG-10-MG-10-MG-10-MG-10-MG-10-MG-10-MG-10-MG-10-MG-10-MG-10-MG-10-MG-10-MG-10-MG-10-MG-10-MG-10-MG-10-MG-10-MG-10-MG-10-MG-10-MG-10-MG-10-MG-10-MG-10-MG-10-MG-10-MG-10-MG-10-MG-10-MG-10-MG-10-MG-10-MG-10-MG-10-MG-10-MG-10-MG-10-MG-10-MG-10-MG-10-MG-10-MG-10-MG-10-MG-10-MG-10-MG-10-MG-10-MG-10-MG-10-MG-10-MG-10-MG-10-MG-10-MG-10-MG-10-MG-10-MG-10-MG-10-MG-10-MG-10-MG-10-MG-10-MG-10-MG-10-MG-10-MG-10-MG-10-MG-10-MG-10-MG-10-MG-10-MG-10-MG-10-MG-10-MG-10-MG-10-MG-10-MG-10-MG-10-MG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: WILLADSEN, Peter
APPLICANT: KEMP, David Harold
APPLICANT: REMP, David Harold
APPLICANT: RIBING, George Alfred
APPLICANT: RAND, Keith No. 6235283man
TITLE OF INVENTION: DNA Encoding A Cell Membrane
TITLE OF INVENTION: Glycoprotein Of A Tick Gut
NUMBER OF SEQUENCES: 71
CORRESPONDENCE ADDRESS:
           ä
           0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       60042/152
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MOORE, Joanna Terry
JOHNSON, Law Anthony York
                                                                                                                                                                                                                                                                                                                US-08-461-004A-56; Sequence 56, Application US/08461004A; Patent No. 6235283; GENERAL INPORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER: 60
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202 672 5300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEX: 904136
INFORMATION FOR SEQ ID NO: 56:
SEQUENCE CHARACTERISTICS:
LENGTH: 650 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            : 3000 K Street, N.W. Washington, D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Foley & Lardner
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  202 672 5399
               5; Conservative
                                                                                                                                                              147 CVPTTC 152
                                                                                   1 CVPLTC 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT:
APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STREET:
               Matches
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us-09-761-636a-12.open.rai

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ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                    MOLECULE TYPE: protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                              1 CVPLTC 6
                                                                                                                                                                                                                                                   TYPE: amir
TOPOLOGY:
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                                                                                                                                                                                                                                                                                                               US-08-461-004A-63
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US-08-461-004A-67
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTY: WEALININGTON, D.C.
CULITI WASHINGTON, D.C.
ZIP: 20007-5109
COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN PC-DOS/MS-DOS
SOFTWARE: PATENTIN PC-DOS/MS-DOS
SOFTWARE: PATENTIN NUMBER: US/08/461,004A
FILING DATE: 04-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/325,071
FILING DATE: 19-OCT-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/AU87/00401
FILING DATE: 27-NOV-1987
FILING APPLICATION DATA:
APPLICATION NUMBER: AU P14912
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: COBON, Stewart Gary
APPLICANT: MOORE, Joanna Terry
APPLICANT: MOORE, Joanna Terry
APPLICANT: WILLADSEN, Law Anthony York
APPLICANT: WILLADSEN, Peter
APPLICANT: KEMP, David Harold
APPLICANT: RIDING, George Alfred
APPLICANT: RIDING, George Alfred
APPLICANT: RAND, Keith No. 6235283man
TITLE OF INVENTION: DNA Encoding A Cell Membrane
TITLE OF INVENTION: Glycoprotein Of A Tick Gut
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 63, Application US/08461004A Patent No. 6235283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE: 16-OCT-1987
PRIOR APPLICATION DATA:
APPLICATION NUMBER: AU PI2570
FILING DATE: 19-JUN-1987
PRIOR APPLICATION DATA:
APPLICATION NUMBER: AU PH9196
FILING DATE: 27-NOV-1986
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          UMBER: AU P14912
16-OCT-1987
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W.
CITY: Washington, D.C.
                                                                                    : 650 amino acids
amino acid
               TELEX: 904136
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                             Query Match
Best Local Similarity 83.3.
  202 672 5399
                                                                                                                          TOPOLOGY: linear
HOLECULE TYPE: protein
US-08-461-004A-59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                            147 CVPTTC 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
APPLICANT: COBON,
                                                                                                                                                                                                                                                                                                      1 CVPLTC 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 12
US-08-461-004A-63
TELEFAX:
                                                                                LENGTH:
                                                                                                           TYPE:
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Gaps
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Pred. No. 4.4e+02;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 67, Application US/08461004A
| Patent No. 6235283
| CENERAL INFORMATION:
| APPLICANT: COBON, Stewart Gary
| APPLICANT: COBON, Law Atthony York
| APPLICANT: WILLADSEN, Law Atthony York
| APPLICANT: WILLADSEN, Peter
| APPLICANT: KEMP, David Harold
| APPLICANT: RIDING, George Alfred
| APPLICANT: RIDING, George Alfred
| APPLICANT: RIDING, George Alfred
| APPLICANT: RAND, Keith No. 6235283man
| TITLE OF INVENTION: Glycoprotein Of A Tick Gut
| NUMBER OF SEQUENCES: 71
| CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CONDITY: USA

ZUDURTY: USA
ZUOUTAY: USA
ZUOUTAY: USA
ZUOUTAY: USA
ZUOUTAY: USA
ZUOUTAY: LEBABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
RING APPLICATION DATA:
APPLICATION NUMBER: US 08/062,109
FILING DATE: 17-MAY-1993
PROM APPLICATION NUMBER: US 08/062,109
FILING DATE: 07-AUG-1992
PRICH APPLICATION NUMBER: 07/42,196
FILING DATE: 06-JUL-1988
PRICH APPLICATION NUMBER: 07/42,196
FILING APPLICATION NUMBER: O7/42,196
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REGISTRATION NUMBER: 60042/152
TELECOMMUNICATION:
TELEPHONE: 202 672 5390
TELEFAX: 202 672 5399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PCT/AU87/00401
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STREET: 3000 K Street, N.W. CITY: Washington, D.C. COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Foley & Lardner
                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 83.3%;
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: PCT/AU FILING DATE: 27-NOV-1987 PRIOR APPLICATION DATA: APPLICATION NUMBER: AU P14 FILING DATE: 16-OCT-1987
                                                                                                                                     TELERAX: 202 672 5399
TELEX: 904136
INFORMATION FOR ESC ID NO: 6
SEQUENCE CHARACTERISTICS:
LENGTH: 650 amino acids
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Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
APPLICANT: COBON, Stewart Gary
APPLICANT: COBON, Stewart Gary
APPLICANT: MOORE, Joanna Terry
APPLICANT: MILLADSEN, Peter
APPLICANT: SKISKANTHA, Alagacone
APPLICANT: RIDING, George Alfred
APPLICANT: RADING, George Alfred
APPLICANT: RADIN, Keith No. 6235283man
TITLE OF INVENTION: DNA Encoding A Cell Membrane
TITLE OF INVENTION: Glycoprotein Of A Tick Gut
NUMBER OF SEQUENCES: 71
CORRESPONDENCE ADRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ZIP: 20007-5109
COMPUTER READABLE PORM:
MEDIUM TYRE: Floppy disk
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRAT APPLICATION DATA:
                                      FILING DATE: 16-OCT-1987
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 40 P12570
FILING DATE: 19-JUN-1987
PRIOR APPLICATION DATA:
APPLICATION NUMBER: AU F19196
FILING DATE: 27-NOV-1986
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REGISTRATION NUMBER: 29,768
REGISTRATION NUMBER: 20,768
TELECOMMUNICATION INFORMATION:
TELECHOME: 202 672 5399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PULLING DATE: US/08/461,004A PILLING DATE: 04-JUN-1995 PRICATION NUMBER: US/08/461,004A PRICATION DATE: APPLICATION NUMBER: US 08/325,071 PILLING DATE: 19-OCT-1994 PRICATION APPLICATION NUMBER: US 08/062,109 PILLING DATE: 17-MAY-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US 07/926,368 FILING DATE: 07-AUG-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-08-461-004A-57; Sequence 57, Application US/08461004A; Patent No. 6235283
                 APPLICATION NUMBER: AU PI4912
FILING DATE: 16-OCT-1987
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: Foley & Lardner STREET: 3000 K Street, N.W. CITY: Washington, D.C.
                                                                                                                                                                                                                                                                                                                                                                                  TELEX: 904136
INFORMATION FOR SEQ ID NO: 57
SEQUENCE CHARACTERISTICS:
LNGTH: 688 amino acids
TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 86.8
Best Local Similarity 83.3
Matches 5; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   157 CVPTTC 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 CVPLTC 6
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SCENALARY STAIRS.
SCENALARY STAIRS.
SCENAL SEASON STAIRS.
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/325,071
FILING DATE: 14-0CT-1993
FRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/062,109
FILING DATE: 17-MAY-1993
FRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/926,368
FILING DATE: 07-MG-1992
FILING DATE: 07-MG-1992
PRICK APPLICATION DATA:
APPLICATION NUMBER: 07/242,196
FILING DATE: 06-UUL-1988
PRICK APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
FILING DATE: 27-NOV-1987
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 57, Application US/08325071
; Sequence 57, Application US/08325071
; Patent No. 5587311
; GENERAL INFORMATION:
APPLICANT: MCORE, Joanna Terry
APPLICANT: WCORE, Joanna Terry
APPLICANT: WILLADSEN, Peter
APPLICANT: KILLADSEN, Peter
APPLICANT: KILLADSEN, Peter
APPLICANT: KILLADSEN, Peter
APPLICANT: RAMP, Alagacone
APPLICANT: RAND, Keith No. 5587311man
TITLE OF INVENTION: DNA Encoding A Cell Membrane
TITLE OF INVENTION: Glycoprotein Of A Tick Gut
NUMBER OF SEQUENCES: 71
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 33; DB 3; Red. No. 4.4e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Mismatches
PRIOR APPLICATION DATA:
APPLICATION NUMBER: AU P12570
FILING DATE: 19-JUN-1987
PRIOR APPLICATION DATA:
APPLICATION NUMBER: AU PH9196
FILING DATE: 27-NOV-1986
ATTONNEY/AGENT INFORMATION:
NAME: BENY, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 60042/152
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202 672 5300
TELEPHONE: 202 672 5300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CITY: Washington, D.C.
CCUNTRY: USA
ZIP: 2007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
COMPATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Foley & Lardner
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  : 3000 K Street, N.W. Washington, D.C.
                                                                                                                                                                                                                                                                                                TELEFAX: 202 672 5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 67
SEQUENCE CHARACTERISTICS:
LENGTH: 650 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-461-004A-67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 83.3%;
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                147 CVPTTC 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 CVPLTC 6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-08-325-071-57
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Search completed: September 5, 2004, 10:22:00 Job time : 6.33333 secs

1 CVPLTC 6 ||| || 157 CVPTTC 162

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GenCore version 5.1.6
(c) 1993 - 2004 Compugen Ltd.
                Copyright
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- protein search, using sw model OM protein

5, 2004, 09:47:29 ; Search time 7.67677 Seconds September Run on:

(without alignments) 125.302 Million cell updates/sec

US-09-761-636A-13 56 1 CISVPLSVPC 10 Title: Perfect score: Sequence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

Searched:

Total number of hits satisfying chosen parameters: 283366 segs, 96191526 residues

seq length: 0 seq length: 200000000 Minimum DB Maximum DB

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR 78:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

hypothetical prote hypothetical prote IMP dehydrogenase IMP dehydrogenase hypothetical prote hypothetical prote sulfated surface g hypothetical prote hypothetical prote hypothetical prote SH2 domain-contain omega-3 fatty acid origin recognition DNA repair protein Ly6 homolog RK3 pr hypothetical prote conserved hypothet probable amino aci probable steroid 2 masC protein - Myc probable aminotran transcription fact probable acyl-coAs acyl-CoA synthetas probable acyl-CoA Description SUMMARIES T44555 G82599 F86298 JC4999 D71864 F82521 A33647 846742 F72751 JC7593 383136 375515 r08827 [49529 115039 **T50982** D75437 Query Match Length DB Score Result No.

hypothetical prote agitoxin 3 - scorp acetate kinase (Ac hypothetical prote probable Prs systeregulatory protein regulatory protein hypothetical prote probable secreted hypothetical prote gene Brn-3b protei	transcription fact protein C (activat hypothetical prote hypothetical prote propanediol dehydr
B97852 C54471 D97718 H71023 AD0966 S06314 F89914 F89914 AD2559 138502	148291 KXHU C95349 H85135 JE0303
000000000000	N 10 10 10 10 10 10 10 10 10 10 10 10 10
1162 38 156 249 250 252 328 3399 4110	440 502 527 554
600.7.7.5 600.7.7.7.5 600.7.7.7.7.5 600.7.7.7.7.7.7.7.7.7.7.7.7.7.7.7.7.7.7.	60.7 60.7 60.7 60.7
N 4 4 4 4 4 4 4 4 4 4 6 6 6 6 6 6 6 6 6	1 61 61 61 1 4 4 4 4
6 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4	4 4 4 4 4 4 5 5 5 5 5 5 5 5 5 5 5 5 5 5

ALIGNMENTS

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hypothetical protein PA0631 [imported] - Pseudomonas aeruginosa (strain PAO1)

C;Species: Pseudomona acruginosa C;Date: 31-Jan-2000 #sequence_revision 31-Jan-2000 #text_change 06-Oct-2000 C;Accession: T44555; E8358 R;Nakayama, K; Takashima, K; Ishihara, H.; Shinomiya, T.; Kageyama, M.; Kanaya, S.; Ob submitted to the EMBL Data Library, August 1999 A;Description: Genetic relationship between bacteriocins and bacteriophages. A;Accession: T44555

A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Status: 1-85 AMEN:
A;Residues: 1-85 AMEN:
A;Cross-references: EMBL:AB030825; PIDN:BAA83170.1
A;Experimental source: strain PAO!
A;Experimental source: strain PAO!
B;Experimental source: strain PAO!
B;Experimental source: strain PAO:
A;Experimental source: strain PAO:
B;Experimental Strain PAO:
B;Experimental Strain PAO:
B;Experimental Strain PAO:
B;Experimental PAO:

GB:AE004091; NID:99946491; PIDN:AAG04020.1; GSPDB:GN001 A;Cross-references: GB:AE004498; G: A;Experimental source: strain PAO1 Genetics

A; Gene: PA0631

; 0 Score 39; DB 2; Length 85; Pred. No. 6; 1; Indels 2; Mismatches 69.68; 6; Conservative Local Similarity Query Match Best Loc Matches

0;

Gaps

2 ISVPLSVPC 10 27 VEVPLAVPC 35 ò g

RESULT 2 G82599

hypothetical protein XF2118 [imported] - Xylella fastidiosa (strain 9a5c)
C;Species: Xylella fastidiosa
C;Species: Xylella fastidiosa
C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 20-Aug-2000
C;Accession: G82590
R;anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Sequen Nature 406, 151-157, 2000
A;Title: The genome sequence of the plant pathogen Xylella fastidiosa.
A;Title: The genome sequence of the plant pathogen Xylella fastidiosa.
A;Note: for a complete list of authors see reference number A59328 below
A;Accession: G82599

probable Acyl-CoA probable single-st

hypothetical hypothetical

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R; Collart, F.R.; Osipiuk, J.; Trent, J.; Olsen, G.J.; Huberman, E. Gene 174, 217-220, 1996 Gene 174, 217-220, 1996 Gene 174, 217-220, 1996 A; Title: Cloning and characterization of the gene encoding IMP dehydrogenase from Arabid A; Reference number: JC4999, MUID: 97045815; PMID: 8890737 A; Accession: JC4999 A; Molecule type: DNA A; Molecule type: DNA A; Molecule type: DNA A; Residues: 1-503 <COL> A; Cross-references: GB: L34684; NID: g1100062; PIDN: AAB41940.1; PID: g1100063
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Description: provides precursors for DNA and RNA biosynthesis; it catalyzes the convex C; Superfamily: IMP dehydrogenase; CBS homology; IMP dehydrogenase amino-terminal homolog C; Keywords: GMP biosynthesis; NAD; oxidoreductase; purine nucleotide biosynthesis from 6.720-86, Domain: IMP dehydrogenase amino-terminal homology <IDHN> F;172-220, Domain: CBS homology <CBS2. F;221-465, Domain: IMP dehydrogenase catalytic homology <IMP>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               hypothetical protein jhp0985 - Helicobacter pylori (strain J99)
hypothetical protein jhp0985 - Helicobacter pylori (strain J99)
kypothetical protein jhp0985 - Helicobacter pylori (strain J99)
kypothetical strain J99
cypecies strain J99
cypecies 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 08-Oct-1999
cypacesion: D71864
kypin, R.A.; Ling, L.S.L.; Moir, D.T.; King, B.L.; Brown, E.D.; Doig, P.C.; Smith, D.R.; Nature 397, 176-180, 1999
kypin, R.A.; Ling, L.S.L.; Moir, D.T.; King, B.L.; Brown, E.D.; Doig, P.C.; Smith, D.R.; Ives, C.; Gibson, R.999
kypin, R.A.; Ling, L.S.L.; Moir, D.T.; King, B.L.; Brown, E.D.; Doig, P.C.; Smith, D.R.; Nature 397, 176-180, 1999
kypin, R.A.; Hille, Genomic sequence comparison of two unrelated isolates of the human gastric pat A; Reference number: A71800; MUD:99120557; PMID:9923682
A; Accession: D71864
A; Residues preliminary
A; Residues 1.-616 cARNA
A; Residues: 1.-616 cARNA
A; Residues: 1.-616 cARNA
A; Residues: 1.-616 cARNA
A; Residues: 1.-616 cARNA
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A;Experimental source: strain J99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Cypothetical protein XF2736 [imported] - Xylella fastidiosa (strain 9a5c)
CySpecies: Xylella fastidiosa
CySpecies: Xylella fastidiosa
CyDate: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 20-Aug-2000
CyAccession: F82521
Ryanonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Seque Nature 406, 151-157, 2000
Ayritle: The genome sequence of the plant pathogen Xylella fastidiosa.
Ayreference number: A82515; MUID:20365717; PMID:10910347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               67.9%; Score 38; DB 1; Length 503; 85.7%; Pred. No. 51; 1.1ve 1; Mismatches 0; Indels
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Osipiuk, J.; Trent, J.; Olsen, G.J.; Huberman,
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C; Complex: homotetramer
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77.8%;
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Best Local Similarity 85.7
Matches 6; Conservative
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A,Status: preliminary
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IMP dehydrogenaee (EC 1.1.1.205) - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar.2001 #sequence_revision 02-Mar.2001 #text_change 17-May-2002
C;Date: 02-Mar.2001 #sequence_revision 02-Mar.2001 #text_change 17-May-2002
C;Accession: F86298
R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; ansen, N.F.; Hudhes, B.; Huizar, L.
Nature 408, 816-820, 2000
A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C. A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, A;Title: Sequence and analysis of Chromosome 1 of the plant Arabidopsis.
A;Reference number: A86141; MUID:21016719; PMID:11130712
A;Residues: 1-502 <STO>
A;Cross-references: GB:AE005172; NID:94966356; PIDN:AAD34687.1; GSPDB:GN00141
                                                                                                                                                                                   A;Experimental source: strain 9a5c
A;Experimental source: strain 9a5c
B;Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.; B
B;Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.; B
B;Simpson, A.J.G.; Reinach, E.C.; Arruda, P.; Abreu, F.A.; Carraro, D.M.; Carrer, H
as-Neto, E.; Docena, C.; Bl-Dorry, H.; Facincani, A.P.; Ferreira, A.J.S.
submitted to GenBank, June 2000
A;Authors: Ferreira, V.C.A.; Ferro, J.A.; Franca, J.S.; Franca, S.C.; Franco, M.C.; Frohm
Chado, M.A.; Madeira, A.M. B.N.; Madeira, H.W.F.; Marrino, C.L.; Marques, M.V.; Martins, F.A;Authors: Martins, E.N.F.; Marsukuma, A.Y.; Marco, B.C.; Miyaki, C.Y.;
F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri, D.P.; Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.B.; de Sa, R.G.; Santelli, R.V.; Sawasak A;Authors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silvaira
A;Contentes annotation
A;Contentes annotation
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C;Keywords: GMP biosynthesis; NAD; oxidoreductase
                                                                                                                                                  A;Cross-references: GB:AE004026; GB:AE003849; NID:g9107228; PIDN:AAF84917.1; GSPDB:GN001
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C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C;Accession: JC4999
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Pred. No. 51;
1; Mismatches
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Pred. No. 10;
3; Mismatches
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50.0%;
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Best Local Similarity 50...
Local Similarity

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Best Local Similarity 85.7
Matches 6; Conservative
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                                 A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-148 <SIM>
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A;Cross-references: GB:M30691; NID:g205251; PIDN:AAA41548.1; PID:g205252
A;Experimental source: clone RK11
C;Superfamily: Ly-6 antigen; Ly-6 homology
C;Superfamily: Ly-6 antigen; Ly-6 homology
F;249yeorstein; phosphatidylinositol linka
F;1-26/Domain: signal sequence #status predicted <AMI>
F;27-105/Product: Ly6 homolog RK3 #status predicted <AMI>
F;106-134/Domain: carboxyl-terminal propeptide #status predicted <AMI>
F;105/Wodified site: GPI-anchor ethanolamine amidated carboxyl end (Asn) (in mature for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             R.Bolotin, A.; Wincker, P.; Mauger, S.; Jaillon, O.; Malarme, K.; Weissenbach, J.; Ehrli
Genome Res. 11, 731-753, 2001
A.Title: The complete genome sequence of the lactic acid bacterium Lactococcus lactis ss
A.Reference number: A86625; MUID:21235186; PMID:11337471
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A;Experimental source: strain R1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nypothetical protein ymhC [imported] - Lactococcus lactis subsp. lactis (strain IL1403)
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T.; Zalewski,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conserved hypothetical protein - Deinococcus radiodurans (strain R1)
C.Species: Deinococcus radiodurans
C.Species: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 17-Mar-2000
C.Accession: G75515
R.White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, M.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.
Science 286, 1571-1577, 1999
A,7Itle: Genome sequence of the radioresistant bacterium Deinococcus radiodurans JA,Rocession: G75515
A,Accession: G75515
A,Accession: G75515
A,Status: preliminary
A,Molecule type: DNA
A,Residues: 1-256 <WHI>
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A;Experimental source: strain IL1403
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C'Species: Lactococcus lactis subsp. lactis
C'Date: 23-Mar-2001 #sequence_revision 23-Mar-2001 #text_change 03-Aug-2001
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                                                                                                                                                                                                                                                                   Length 134;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 36; DB 2
Pred. No. 48;
3; Mismatches
                                                                                                                                                                                                                                                                                                         1; Mismatches
                                                                                                                                                                                                                                                                 Score 36;
                                                                                                                                                                                                                                                                                    Pred. No.
                                                                                                                                                                                                                                                          64.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     64.3%;
55.6%;
                                                                                                                                                                                                                                                                                                       6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                 1 CISVPLSVPC 10
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128 CINLPLOIP 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 CISVPLSVP 9
                                                                                                                                                                                                                                                                                                                                                                                            32 CIEVPLNANC
                                                                                                                                                                                                                                                                             Best Local Similarity
Matches 6; Conserv
                              A; Residues: 2-134 < FR2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1-207 <STO>
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Best Local Similarity
Matches 5; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Accession: B86781
A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C, Accession: B86781
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Map position: 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Gene: DR0471
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Gene: ymhC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Residues:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Loca
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C; Genetics
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Ly6 homolog RK3 precursor - rat
C;Species: Rattus norregicus (Norway rat)
C;Species: Rattus norregicus (Norway rat)
C;Species: Rattus norregicus (Norway rat)
C;Accession: D45835; C45835
R;Friedman, S; Palfree, R.G.E.; Sirlin, S.; Haemmerling, U.
R;Friedman, S.; Palfree, R.G.E.; Sirlin, S.; Haemmerling, U.
A;Title: Analysis of three distinct Ly6-A-related cDNA sequences isolated from rat kidne
A;Reference number: A45835; MUD:90152758; PMID:2154400
A;Residues: 1-134 cFRI>
A;Residues: 1-134 cFRI>
A;Cross-references: GB:M30690; NID:9205249; PIDN:AAA41547.1; PID:9205250
A;Accession: C45835
A;Molecule type: mRNA
A;Roession: C45835
A;Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sulfated surface glycoprotein 185 - Volvox carteri
c)species: Volvox carteri
C;Date: 11-Apr-1990 #sequence_revision 11-Apr-1990 #text_change 21-Jul-2000
C;Date: 11-Apr-1990 #sequence_revision 11-Apr-1990 #text_change 21-Jul-2000
C;Accession: A33647
B;Ertl, H.; Mengele, R.; Wenzl, S.; Engel, J.; Sumper, M.
J. Cell Biol. 109, 3493-3501, 1989
A;Title: The extracellular matrix of Volvox carteri: molecular structure of the cellular
A;Reference number: A33647; MUID:90094551; PMID:2689458
A;Status: preliminary
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A;Residues: 1-485 <ERT>
A;Cross-references: GB:X51616; NID:g21999; PIDN:CAA35953.1; PID:g1405821
C;Keywords: glycoprotein
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Pred. No. 14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             66.1%;
66.7%;
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2 ISVPLSVPC 10 VSAPLRVPC 27

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Query Match Best Local Similarity 6; Conserve

A; Contents: annotation

A; Gene: XF2736

C, Genetics

R.J.; C.; Ma

| :|||: || CQTVPLTEPC 92 1 CISVPLSVPC 10

Best Local Similarity Matches 6; Conserv

ò g

Query Match

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A;Molecule type: DNA
A;Residues: 1-581 <DUZ>
A;Cross_references: EMBL:U00062; NID:g488162; PIDN:AAB68911.1; PID:g488176; MIPS:YHR032v
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         R.Kawarabayasi, Y.; Hino, Y.; Horikawa, H.; Yamazaki, S.; Haikawa, Y.; Jin-no, K.; Taka awa, H.; Zakamiya, M.; Masuda, S.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; DNA Res. 6, 83-101, 1999
A;Title: Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, Aeropy A;Reference number: A72450; MUID:99310339; PMID:10382966
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A,Gene: cotel
A,Map position: 1
A;Introns: 75/3; 94/3; 131/3; 171/3; 207/3; 266/2; 299/3; 323/1; 505/1; 528/1; 612/3
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C;Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 20-Jun-2000
C;Accession: F72751
                         hypothetical protein YHR032w - yeast (Saccharomyces cerevisiae)
N.Alternate names: hypothetical protein H8179.15
C,Species: Saccharomyces cerevisiae
C,Date: 28-Oct-1994 #sequence_revision 28-Oct-1994 #text_change 19-Apr-2002
C,Accession: S46742
S,Du, Z.
Submitted to the RMBL Data Library, May 1994
A,Description: The sequence of S. cerevisiae cosmid 8179.
A,Reference number: S46732
A,Accession: S46742
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 581;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 64.3%; Score 36; DB 2; I 50.0%; Pred. No. 1.3e+02; ive 3; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                             A,Cross-references: SGD:S0001074
A,Map position: 8R
C,Keywords: transmembrane protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 50.0
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 70.0
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        139 ČPSVPĽLRPC 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     |:|:|:| |
564 CVSIPVSSGC 573
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 CISVPLSVPC 10
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A; Status: preliminary
A; Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C, Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                            C;Genetics:
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RESULT 13
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                                                                                                                                                                             probable amino acid permease PA4072 [imported] - Pseudomonas aeruginosa (strain PA01) probable s: Pseudomonas aeruginosa (5,5pecies: Pseudomonas aeruginosa (5,5pecies: Pseudomonas aeruginosa (5,5pecies: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000 (5,5cession: G83136 R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, M.J.; Bristover, C.K.; Pham, X.Q.; Erwin, A.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Linker, S. Joson, M.V.
Nature 406, 959-964, 2000 A;Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pathoral A;Reference number: A82950; MUID:20437337; PMID:10984043
A;Reference number: A82950; MUID:20437337; PMID:10984043
A;Residues: 1-496 <STO>A;Residues: 1-496 <STO>A;Residues: 1-496 <STO>A;Residues: 1-496 <STO>A;Cross-references: GB:AE004823; GB:AE004091; NID:99950265; PIDN:AAG07459.1; GSPDB:GN001 A;Experimental source: strain PA01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C;Accession: H96759

R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000

A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C. A; Authors: Hunter, J.L.; Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, E.; Kim, C. A; Liz, M.; Rooney, T.; Rowley, D.; Sakano, H.
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, A;Authors: Salzberg, C.M.; Vonter, J.C.; Davis, R.W.
A;Accession: H96759
A;Accession: H96759
A;Accession: H96759
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               probable steroid 22-alpha-hydroxylase T9L24.44 [imported] - Arabidopsis thaliana C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar_2001 #sequence_revision 02-Mar-2001 #text_change 02-Apr-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
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C,Superfanily: Synechocystis cytochrome P450 slr0574; cytochrome P450 homology
C,Keywords: heme; iron; metalloprotein
F;455/Binding site: heme iron (Cys) (axial ligand) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Molecule type: DNA
A;Realdues: 1-512 <STO>
A;Cross-references: GB:AE005173; NID:g11120803; PIDN:AAG30983.1; GSPDB:GN00141
C;Genetics:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 496;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 36; DB 2; Length 496
Pred, No. 1.1e+02;
3; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 64.3%;
Best Local Similarity 50.0%;
Matches 5; Conservative 3
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                                                              CVPAPRSAPC 13
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           CISVPLSVPC
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A;Residues: 1-100 <KAW>

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A;Cross-references: DDBJ:AP000058; NID:g5103388; PIDN:BAA78912.1; PID:g5103391
A;Experimental source: strain Kl
C;Genetics:
A;Gene: APE0003
C;Superfamily: Aeropyrum pernix hypothetical protein APE0003
```

0; Gaps Query Match
Best Local Similarity 71.4%; Pred. No. 35;
Matches 5; Conservative 2; Mismatches 0; Indels

0

4 VPLSVPC 10 :||:||| 57 IPLTVPC 63

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Search completed: September 5, 2004, 10:01:24 Job time : 9.67677 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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OM protein - protein search, using sw model

September 5, 2004, 09:38:39 ; Search time 4.54545 Seconds (without alignments)
114.554 Million cell updates/sec Run on:

US-09-761-636A-13 56 1 CISVPLSVPC 10

Title: Perfect score: Sequence:

Scoring table:

141681 segs, 52070155 residues BLOSUM62 Gapop 10.0 , Gapext 0.5

Total number of hits satisfying chosen parameters: Searched:

141681

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt_42:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		Description		of piromyce	arahidonei	arabidonei			P21997 volvox cart	sacchar				mus		fowlpox								012837 homo sanien					Ogenal homo sanien	Tan T			Omor oppe	60015 nen +	3092	
N N			1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1																																	
SUMMARIES		ID	MANC PIRSP	MANB_PIRSP	IMH2 ARATH	IMH1 ARATH	Y396 HELPJ	CG2A CHLVR	SSGP_VOLCA	YHJ2 YEAST	COTE_HUMAN	YMA2 MYCBO	MAFB HUMAN	MAFB_MOUSE	MAFB_RAT	V181 FOWPV	FD21 MYCTU	FD21 MYCLE	KCH2 CANFA	SY23 HUMAN	SCA3 LEIOH	LUXR VIBFI	V027 FOWPV	PO42 HUMAN	RTC1_DICDI	PRIC HUMAN	DHAB SALTY	MP44 SFVKA	SILL HUMAN	SILL PANTR		CADG HUMAN	OPSB_HUMAN	OPSB_PANTR	1 1	
		DB	-	н		-	П	Н	Н	Н	н	П	_	Н	7	П	Н	-	Н	Н	7	Н		-	-	-	Н	-	7	П	-	٦	н	-	щ	
		Length	569	571	502	503	616	420	485	581	699	298	323	323	323	369	578	579	1158	120	38	250	336	410	433	461	554	590	595	597	909	829	348	348	349	
æ	Query	Match	5	75.0	6.79	5	5	66.1	•		64.3	•	•		•					9.19	60.7	60.7	60.7	60.7	60.7	60.7	60.7	60.7	60.7	60.7	60.7	60.7	58.9		58.9	
		Score	42	42	38	38	38	37	37	36	36	32	χ. 1.	35	35	35	35	35	m	34.5	34	34	34	34	34	34	34	34	34			34		33		
	Result	No.	н	7	m	4	Ŋ	9	7	ω (. פ	07.	17.	77	T :	14	15	16	17	18	19	20	21	22	23	24	25	56	27	28	59	30	31	32	33	

P54844 rattus norv P23091 avian musculu P54843 mus musculu O75444 homo sapien Q14153 homo sapien P53101 saccharomyc Q91u6 mus musculu P19467 mus musculu Q50586 mycobacceri P58021 mus musculu Q99805 homo sapien P16044 tachypleus	
MAF RAT TWAF AVIS4 MAF WOUSE MAF HUMAN Y140 HUMAN WGT4 YEAST WD23 MOUSE C114 MOUSE FD25 MYCTU T952 MOUSE T952 HUMAN IBPI TACTR	
нанананана	
3699 3769 3769 4403 5749 573 673 673 673 673	
0.000000000000000000000000000000000000	
шппппппч44444 4506789012245	

ALIGNMENTS

DB 1; Length 569;

75.0%; Score 42;

Query Match

Best Local Matches

à g MANB_PIRSP

RESULT 2

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                                                                                                                                                                                                                                                                                                                                 C STRAIN=CV. Columbia;

XX MEDLINE=21016719; PubMed=11130712;
XX Theologis A., Ecker J.R., Falm C.J., Federspiel N.A., Kaul S.,
XX Theologis A., Ecker J.R., Falm C.J., Federspiel N.A., Kaul S.,
XX Theologis A., Ecker J.R., Palm C.J., Forney R.,
XX Mite O., Alonso J., Altafi H., Araujo R., Bowman C.L., Brooks S.Y.,
XX Buehler E., Chan A., Chao Q., Chen H., Cheuk R.F., Chin C.W.,
XX Chung M.K., Conn L., Conway A.B., Creasy T.H., Dewar K.,
XX Dunn P., Ergu P., Feldblyum T.V., Feng J.-D., Fong B., Fujii C.Y.,
XX Hunter J.L., Jenkins J., Johnson-Hopson C., Khan S., Khaykin E.,
XX Kim C.J., Koo H.L., Kremenetskaia I., Kurtz D.B., Kwan A., Lam B.,
XX Liu S.X., Liu Z.A., Luros J.S., Malti R., Marziali A.,
XX Allitscher J., Miranda M., Nguyen M., Nierman W.C., Osborne B.I.,
XX Allits A., Salzberg S.L., Schwartz J.R., Solinn P., Southwick A.M.,
XX Sun H., Tallon L.J., Tambunga G., Toriumi M.J., Town C.D.,
XX W. D., Yu G., Fraser C.M., Venter J.C., Davis R.W.;
XX W. D., Yu G., Fraser C.M., Venter J.C., Davis R.W.;
XX W. D., Yu G., Fraser C.M., Venter J.C., Davis R.W.;
XX Thaliana.",
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HISSP, PIZZ68, 1830.
InterPro: IPR003099; FMN enzyme.
InterPro: IPR005999; IMP_dehyd.
InterPro: IPR001093; IMPDH/GMPRtase.
Pfam; PF00478; IMPDH: 1.
TIGRFMNs: TIGR01302; IMP_dehydrog; 1.
PROSITE; PS00487; IMP_DH_GMP_RED; 1.
Oxidoreductase; NAD; GMP_biosynthesis; Purine biosynthesis; Repeat;
                                                                                                                                                                      Arabidopsis thaliana (Mouse-ear cress).

Bukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.

NCBI_TaxID=3702;
                                                                       16-CCT-2001 (Rel. 40, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Probable inosine-5'-monophosphate dehydrogenase (EC 1.1.1.205) (IMP
Gehydrogenase) (IMPDH) (IMPDH) (IMPDH)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "ALTE 408:816-820(2000).

"Attree 408:816-820(2000).

-!- CATALYTIC ACTIVITY: Inosine 5'-phosphate + NAD(+) + H(2)O = xanthosine 5'-phosphate + NADH.

-!- PATHWAY: First reaction unique to GMP biosynthesis.

-!- SIMILARITY: Belongs to the IMPDH/GMPR family.

-!- SIMILARITY: Contains 1 CBS domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 1; Length 502;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               54051 MW; FB87D84160818310 CRC64;
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1; Mismatches
         502 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 67.9%; Score 38;
           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IMP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL, ACO06341; AAD34687.1; -. PIR; F86298; F86298. HSSP, P12268; 1830.
                                                       40, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           6; Conservative
             STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          219
                                                                                                                                               dehydrogenase) (IMPDH
ATIG16350 OR F309.15.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 321 3
502 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4 VPLSVPC 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              |||:||
49 VPLSIPC
                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              167
                                                     16-OCT-2001
16-OCT-2001
           IMH2 ARATH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
                ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Evidence that the Piromyces gene family encoding endo-1,4-mannanases arose through gene duplication.";
FEMS Microbiol. Lett. 141:183-184 (1996).
-!- CATALYTIC ACTIVITY: Random hydrolysis of 1,4-beta-D-mannosidic linkages in mannans, galactomannans, glucomannans, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              galactoglucomannans.
--- SIMILARITY: THE 39 AA REPEATS ARE SIMILAR TO THOSE IN MANA, MANC AND XYNA, AND TO THOSE OF N. PATRICIARUM XYNA.
--- SIMILARITY: Belongs to family 26 of glycosyl hydrolases.
                    Gaps
                                                                                                                                                                                                                                                                                     01-0CT-1996 (Rel. 34, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
Mannan endo-1,4-beta-mannosidase B precursor (EC 3.2.1.78) (Beta-
mannanse B) (1.4-beta-D-mannan mannanohydrolase B).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MANNAN ENDO-1,4-BETA-MANNOSIDASE B. 2 X 39 AA APPROXIMATE REPEATS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .;
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Pred. No. 4.4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
MEDLINE=96313314; PubMed=8768520;
Millward-Sadler S.J., Hall J., Black G.W., Hazlewood G.P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hydrolase; Glycosidase; Signal; Multigene family; Repeat.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3; Indels
                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            B13E44581FAA9DAA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Fungi; Chytridiomycota; Neocallimasticales;
Neocallimasticaceae; Piromyces.
NCBL_TaxID=45796;
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س
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1; Mismatches
Pred. No. 4.3;
                         Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Interpro; IPR002883; Dockerin CBD 5.
Interpro; IPR009034; Dockering CDD.
Interpro; IPR008979; Gal bind Jike.
Interpro; IPR00805; Glyco_hydro_26.
Ffan; PF02013; CBM IO; 2.
Ffan; PF02156; Glyco hydro_26; IPR070159; GLYCO hydro_26; IPR070139; GLYDRIASE26.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    POLY-ASN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                64397 MW;
                                                                                                                                                                                                                                                                       (Rel. 34, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          75.0%;
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  60.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           501
                         Conservative
                                                                                                                                                                                                                           STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 CISVPLSVPC 10
                                                                                                            490 ĆFŚIPĽGYPC 499
                                                                     10
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CFSIPLGYPC
                                                                     1 CISVPLSVPC
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    Similarity
                                                                                                                                                                                                                                                                                                                                                                                                        Piromyces sp
                                                                                                                                                                                                                      MANB PIRSP
P55297;
                                                                                                                                                                                                                                                                     01-0CT-1996
                         .,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                492
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Gaps

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Indels

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DOMAIN

REPEAT DOMAIN DOMAIN

Matches

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RESULT 3

SIGNAL

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CBS domain.
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                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROW N.A.

SC STRAIN=cv. Columbia,

RA MEDINE=21016719; PubMed=11130712;

RA Moltogis A., Ecker J.R., Palm C.J., Federspiel N.A., Kaul S.,

RA White O., Alonso J., Altafi H., Araujo R., Bowman C.L., Brooks S.Y.,

RA Buehler E., Chan A., Chao Q., Chen H., Cheuk R.F., Chin C.W.,

Chung M.K., Conn L., Conway A.B., Conway A.R., Creasy T.H., Dewar K.,

RA Dunn P., Etgu P., Feldblyuw T.V., Feng J.-D., Fong B., Fujii C.Y.,

RA Gill J.E., Goldsmith A.D., Haas B., Hansen N.F., Hughes B., Huizar L.,

RA Hunter J.L., Jenkrins J., Johnson-Hopson C., Khan S., Khaykin E.,

RA Langin-Hooper S., Lee A., Lee J.M., Lenz C.A., Li J.H., Li Y.-P.,

RA Langin-Hooper S., Lee A., Lee J.M., Neuran W.C., Osborne B.I.,

RA Langin-Hooper S., Low A., Lurso J.S., Maiti R., Marziali A.,

RA Miltscher J., Miranda M., Nguyen M., Nieuran W.C., Osborne B.I.,

RA Salzberg S.L., Schwartz J.R., Shinn P., Southwick A.M.,

RA Utterback T., Van Aken S., Vasberg M., Vysotskaia V.S., Walker M.,

RA Wu D., Yu G., Fraser C.M., Venter J.C., Davis R.W.;

RA Wu D., Yu G., Fraser C.M., Venter J.C., Davis R.W.;

RA Wu D., Yu G., Fraser C.M., Venter J.C., Davis R.W.;

RA H. Sequence and analysis of chromosome 1 of the plant Arabidopsis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its most by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
STRAIN=cv. Columbia;
MEDLINE=97045815; PubMed=8890737;
Collart F.R., Osipluk J., Trent J., Olsen G.J., Huberman E.;
"Cloning and characterization of the gene encoding IMP dehydrogenase from Arabidopsis thaliana.";
Gene 174:217-220(1996).
                                                                                                                                                                                        Arabidopsis thaliana (Mouse-ear cress).

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.

NCBI_TaxID=3702;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PROSITE; PS00487; IMP_DH_GMP_RED; 1.
Oxidoreductase; NAD; GMP_biosynthesis; Purine biosynthesis; Repeat;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nature 408:816-820(2000).

-!- CATALYTIC ACTIVITY: Inosine 5'-phosphate + NAD(+) + H(2)O xanthosine 5'-phosphate + NADH.

-!- PATHWAY: First reaction unique to GMP biosynthesis.

-!- SIMILARITY: Belongs to the IMPDH/GMPR family.

-!- SIMILARITY: Contains 2 CBS domains.
                                                                                     01-FEB-1996 (Rel. 33, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Inosine-5'-monophosphate dehydrogenase (EC 1.1.1.205) (IMP
                                                            503 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR003009; FMN enzyme.
InterPro; IPR005990; IMP_dehyd.
InterPro; IPR001099; IMPDh/GMPRtase.
Pfam; Pr00478; IMPDH; IMP dehydrog; ITGRFAMS; TIGR01302; IMP dehydrog; I.
PROSITE; PS00487; IMP_DH-GMP_RED; I.
                                                          PRT;
                                                                                                                                                            dehydrogenase) (IMPDH) (IMPD).
IMPDH OR AT1G79470 OR T8K14.11.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; AC007202; AAD30229.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; L34684; AAB41940.1;
                                                          STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PIR, JC4999, JC4999.
HSSP, P12268; 1B30.
                                                        IMH1_ARATH
P47996;
                                        IMH1_ARATH
                       RESULT 4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ;
0
                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Alm R.A., Ling L.-S.L., Moir D.T., King B.L., Brown E.D., Doig P.C., Smith D.R., Noonan B., Guild B.C., deJonge B.L., Carmel G., Tummino P.J., Caruso A., Uria-Nickelsen M., Mills D.M., Ives C., Giber R., Merberg D., Mills S.D., Jiang Q., Taylor D.E., Vovis G.F.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Helicobacter pylori J99 (Campylobacter pylori J99).
Bacteria, Proteobacteria, Epsilonproteobacteria, Campylobacterales,
Helicobacteraceae, Helicobacter.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Genomic sequence comparison of two unrelated isolates of the human gastric pathogen Helicobacter pylori.";
Nature 397:176-180(1999).
-!- SIMILARITY: Belongs to the ubiD family.
                                                                                                                   ·.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ..
0
                                                                     Length 503;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 38; DB 1; Length 616;
Pred. No. 24;
                                                                                                                 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                       503 AA; 54194 MW; ADDDAF9C3A697A9A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hypothetical protein; Complete proteome.
SEQUENCE 616 AA; 70989 MW; C219ElDCE4C8BDD5 CRC64;
                                                                   DB 1;
20;
                                                                                                                                                                                                                                                                                                                                                      30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
16-CCT-2001 (Rel. 40, Last annotation update)
Hypothetical protein JHP0985.
    IMP (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-0CT-1996 (Rel. 34, Created)
01-0CT-1996 (Rel. 34, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
CALOrohydra viridissima (Hydra).
                                                                                                                                                                                                                                                                                                                   616 AA.
                                                                                                               1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  420 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
                                                                67.9%; Score 38; 85.7%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL, AE001527; AAD06568.1; -.
PIR, D71864; D71864
Interpro; IPR002830; carboxylyase.
Pfam; PP01977; UbiD; I.
TIGRFAMS; TIGR00148; I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=99120557; PubMed=9923682;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 67.9%;
                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                               STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity 77.8
nes 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              253 CLŚNPLSVP 261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      6
                                                                                                                                                      4 VPLSVPC 10
                                                                                   Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 CISVPLSVP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI TaxID=85963;
                                                                                                                                                                                    |||:||
49 VPLSIPC
                                                                                                                                                                                                                                                                                        Y396_HELPJ
ID _Y396_HELPJ
BINDING
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CHLVR
                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CG2A_CHL7
P51986;
                                                                                                                                                                                                                                                                                                                               Q9ZKF3
                                                                                          Best Loc
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CG2A_CHLVR
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                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
STRAIN=S288C / AB972;
STRAIN=S288C / AB972;
STRAIN=S288C / AB972;
MEDLINE=943708003; PubMed=8091229;
Johnston M., Andrews S., Brinkman R., Cooper J., Ding H., Dover J.,
Johnston M., Andrews S., Brinkman S., Geisel C., Kirsten J.,
Kucaba T., Hillier L.W., Jier M., Johnston L., Langston Y.,
Latreille P., Louis E.J., Macri C., Mardis E., Menezes S., Mouser L.,
Nhan M., Rifkin L., Riles L., St Peter H., Trevaskis E., Vaughan K.,
Vignati D., Wilcox L., Wohldman P., Waterston R., Wilson R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       'Complete nucleotide sequence of Saccharomyces cerevisiae chromosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Science 265:2077-2082(1994).
-!- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
-!- SIMILARITY: Belongs to the multi antimicrobial extrusion (MATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Saccharomyces cerevisiae (Baker's yeast).
Eukaryota, Fungi, Ascomycota, Saccharomycotina, Saccharomycetes;
Saccharomycetales, Saccharomycetaceae, Saccharomyces.
PTM: Hydroylated on proline residues in the Pro-rich central
                                                                                                                                                                                                                                                                                                                                                                                        POLY-PRO.
N-LINKED (GLCNAC. . .) (POTENTIAL)
N-LINKED (GLCNAC. . .) (POTENTIAL)
                                                                                                                                                                                                                                                                                                                 POTENTIAL.
SULFATED SURFACE GLYCOPROTEIN 185.
PRO-RICH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-FEB-1995 (Rel. 31, Created)
01-FEB-1995 (Rel. 31, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Hypothetical 64.2 kDa protein in SLT2-PUT2 intergenic region.
                                        contains sulfate-substituted glycans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 37; DB 1; Length 485;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                  A52216400A031421 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    581 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pred No.
                                                                                                                                                                                                                                                                                                      Signal; Glycoprotein; Hydroxylation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         50436 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; U00062; AAB68911.1; -. PIR; S46742; S46742.
                                                                                                                                                                                                                                                              EMBL; X51616; CAA35953.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 66.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   60.08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
                                                                                                                                                                                                                                                                                                                                                340
340
193
347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 CISVPLSVPC 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            83 COTVPLTEPC 92
                                                 -!- PTM: Glycosylated;
                                                                                                                                                                                                                                                                                                                                                21
228
260
193
347
485 AA;
                                                                                                                                                                                                                                                                                    PIR; A33647; A33647
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=4932;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         YHJ2 YEAST
P38767;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             family
                                                                                                                                                                                                                                                                                                                                                                                                                 CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                       CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
                                                                                                                                                                                                                                                                                                                                 SIGNAL
                                                                                                                                                                                                                                                                                                                                                                           DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                               DOMAIN
                                                                                                                                                                                                                                                                                                                                                       CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       YHJ2_YEAST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               qq
      à
                                                                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lab-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SUBUNIT: Polymer.
PTM: Intersubunit cross-links are formed between saccharide chains
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           the cellular compartment.";
J. Cell Biol. 109:3493-3501(1989).

-i. Cell Biol. 109:3493-3501(1989).

-i. FUNCTION: The extracellular matrix (ECM) of volvox contains insoluble fibrous layers that surround individual cells at a distance to form contiguous cellular compartments. SSG 185 is the monomeric precursor of this substructure (C3Z structure).
                                                                                                                                                                                                          J. Cell Sci. 109:1063-1069(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ð
                                                                                                                                                                                                                                              (mitosis) translition. Interacts with the CDC2 and CDK2 protein kinases to form MPF. G2/M cyclins accumulate steadily during G2 and are abruptly destroyed at mitosis (By similarity).
                                                                                                                                                                                  "Presence and expression of G2 cyclins in the coelenterate hydra.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
STRAIN=f. Nagariensis / HK10;
BIRDILINE=90094551; PubMed=2689458;
Ertl H., Mengele R., Menzl S., Engel J., Sumper M.;
"The extracellular matrix of Volvox carteri: molecular structure
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2;
             Eukaryota; Metazoa; Cnidaria; Hydrozoa; Hydroida; Anthomedusae;
                                                                                                                          MEDLINE=96338615; PubMed=8743953;
Scheurlen-Blchle I., Hoffmeister S., Herrmans-Borgmeyer I.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 37; DB 1; Length 420;
Pred. No. 25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sulfated surface glycoprotein 185 precursor (SSG 185).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    420 AA; 47989 MW; 79225BF8D1B44788 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (Rel. 19, Created)
(Rel. 19, Last sequence update)
(Rel. 43, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    485 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SMART; SM0385; CYCLIN; 2.
PROSITE; PS00292; CYCLINS; 1.
Cyclin; Cell cycle; Cell division; Mitosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   rather than between polypeptide chains
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR006670; Cyclin.
InterPro; IPR004367; Cyclin_Cterm.
InterPro; IPR006671; Cyclin_N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                66.1%;
58.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pfam; PF00134; cyclin; 1. Pfam; PF02984; cyclin_C; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; X90983; CAA62470.1; -. HSSP; P30274; IVIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           408 CVSSLVPLEMPC 419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 CIS--VPLSVPC 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
                                          Hydridae; Chlorohydra.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Volvocaceae; Volvox.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity
                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=3067;
                                                         NCBI_TaxID=6082;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Volvox carteri
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-AUG-1991
01-AUG-1991
15-MAR-2004
                                                                                                                                                                       Schaller H.C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VOLCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      P21997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NON TER
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TISSUE=Hippocampus;
MEDLINE=97474796; PubMed=9331372;
Winfield S.L., Tayebi N., Martin B.M., Ginns E.I., Sidransky E.;
"Identification of three additional genes contiguous to the
glucocerebrosidase locus on chromosome 1q21: implications for Gaucher
disease.";
                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -!- SUBCELLUIAR LOCATION: Integral membrane protein (Potential).
-!- TISSUE SPECIFICITY: Widely expressed.
-!- SIMILARITY: TO HUMAN KIAA0574.
                                                                                                                                                                                                 .
0
                                                                                                                                                                      Score 36; DB 1; Length 581;
Pred. No. 53;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 36; DB 1; Length 669;
Pred. No. 61;
0; Mismatches 3; Indels
                                                                                                                                                                                                2; Indels
                                                                                                                                           B0592C480589319B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                E30360AC9A4571E6 CRC64;
                                                                 Transmembrane; Transport.
                                                                                                                                                                                                                                                                                                                                    30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                 669 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PIR; T08827; T08827.
Genew; HGNC:1233; Clorf2.
GO; GO:0016021; C:integral to membrane; NAS.
                                                                                                                                                                                                3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          or send an email to license@isb-sib.ch).
                                                                                                                   POTENTIAL.
                                                                                            POTENTIAL.
                                                                                                       POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  POTENTIAL. POTENTIAL.
                                                                                                                                POTENTIAL
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POLY-SER.
                                                                                                                                                                                                                                                                                                               PRT;
                                                                                                                                           64209 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; AF023268; AAC51822.1; -.
                                                  TIGRFAMS; TIGR00797; matE; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Genome Res. 7:1020-1026(1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                71482 MW;
                                                                                                                                                                      64.38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         64.3%;
                                                                                                                                                                                 50 08;
GermOnline; 139349; -.
SGD; S0001074; YHR032W.
InterPro; IPR002528; MatE.
Pfam; PF01554; MatE; 2.
                                                                                                                                                                                Best Local Similarity 50 (Matches 5; Conservative
                                                                                                                                                                                                                                                                                                               STANDARD;
                                                                                      302
302
366
492
                                                                                                                                                                                                                                     |:|:| |
564 CVSIPVSSGC 573
                                                                                                                                                                                                                      1 CISVPLSVPC 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     54
87
1111
194
250
639
                                                              Hypothetical protein;
TRANSMEM 173 193
                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens (Human).
                                                                                                                                           581 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    244
635
669 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                        249
282
346
472
                                                                                                                                                                                                                                                                                                                                                                                           OR COTE1
                                                                                                                                                                                                                                                                                                                                                                            COTE1 protein.
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                                                                                                                                                                                                                                                                                                               COTE HUMAN
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TRANSMEM
                                                                                        TRANSMEM
                                                                                                    TRANSMEM
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                                                                                                                              PRANSMEM
                                                                                                                                          SEQUENCE
                                                                                                                                                                    Query Match
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                                                                                                                                                                                                                                                                                    RESULT 9
COTE HUMAN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TISSUE-Bone marrow;
MEDLINE-99375320; PubMed=10444328;
Mang P.W., Eisenbart J.D., Cordes S.P., Barsh G.S., Stoffel M.,
Le Beau M.M.,
"Human KRML (MAPB): cDNA cloning, genomic structure, and evaluation as
a candidate tumor suppressor gene in myeloid leukemias.";
                                                                                                                                                                                                                                                                                                                                                                                 from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                       Mathur M., Kolattukudy P.E.;
"Molecular cloning and sequencing of the gene for mycocerosic acid
synthase, a novel fatty acid elongating multifunctional enzyme, fro
Mycobacterium tuberculosis var. bovis Bacillus Calmette-Guerin.";
J. Biol. Chem. 267:19388-19395(1992).
-! SIMILARITY: STRONG, TO M.TUBERCULOSIS RV1521.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q9Y5G3; Q9HIPI;
28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
10-0CT-2003 (Rel. 42, Last annotation update)
Transcription factor MafB (V-maf musculoaponeurotic fibrosarcoma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .
                                                                                                                                                                                                                            Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hypothetical protein, Transmembrane.
SEQUENCE 298 AA; 32286 WW, 22232DD5DBC6F371 CRC64;
                                                                                                                                                                                                                                             Corynebacterineae; Mycobacteriaceae; Mycobacterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ,0
                                                                                                                                         01-JUN-1994 (Rel. 29, Created)
01-JUN-1994 (Rel. 29, Last sequence update)
16-0CT-2001 (Rel. 40, Last annotation update)
Mycobacterium bovis.
                                                                                                               298 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      entities requires a license agreement (St or send an email to license@isb-sib.ch).
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Pred. No.
                                                                                                               PRT;
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                                                                                                                                                                                                                                                                                                        STRAIN=BCG;
MEDLINE=92406887; Pubmed=1527058;
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Pfam; PF00501; AMP-binding; 1.
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Local Similarity 87.5%;
Les 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; M95808; AAA25367.1;
                                                                                                              STANDARD;
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                            139 CPSVPLLRPC 148
1 CISVPLSVPC 10
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                                                                                                                                                                                                                                                            NCBI_TaxID=1765;
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                                                                                                              YMA2 MYCBO
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                                                                             RESULT 10
YMA2 MYCBO
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Matches
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Gaps

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Best Local Similarity 70.0 Matches 7; Conservative

Genew; HGNC:6408; MAFB.

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                          RX Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Ratausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Schuler G.D., Atausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D., Atausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D., Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Atacheron E.P., Wang J., Hsieh F., Jaccheron H., Moore T., Max S.I., Wang J., Hsieh F., Anderden M.J., Usdin T.B., Poraldo M.F., Casavant T.L., Scheetz T.E., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., Raha S.S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., R. Hohards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Allalon D.K., Muzry D.M., Sodergren E.J., Lu X., Gibbs R.A., Anders S., Worley K.C., Shevchenko Y., Bouffard G.G., Rakesley R.W., Touchman J.W., Green E.D., Dickson M.C., A Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., A Brakesley R.W., Touchman J.W., Green E.D., Dickson M.C., A Brakesley R.W., Touchman J.W., Green E.J., Dickson M.C., A Schnerch A., Schmitz J., Marra M.A., Schnist A., Schmitz J., Marra M.A., Schnist J., Jones S.J.M., Marra M.A., Former chan intital analysis of more than 15,000 full-length human and mouse cDNA sequences.", Thuman and mouse cDNA sequences.", Thuran M.A., Schelland R.G., Thuman and mouse cDNA sequences.", Thuran M.A., Schelland R.G., Thuman and mouse cDNA sequences.", 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "The DNA sequence and comparative analysis of human chromosome 20."; Nature 414:865-871(2001).
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Genomics 59:275-281(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TISSUE=Brain;
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AREALINE=22388257; PubMed=12477932;

A Etrausher R.D., Feingold E.A., Grouse L.H., Derge J.G.,

A traushers R.D., Collins F.S., Wagner L., Shemmen C.M., Schuler G.D.,

A Itschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

A Alschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

A Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

A Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

A Rapleton M., Soares M.B., Bonaldo M.F., Carainoi P., Prange C.,

A Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

A Raha S.S., Morley K.C., Markernan K.J., Malek J.A., Guaratane P.H.,

A Richards S.W., McEwan P.J., McKernan K.J., Malek J.A., Guaratane P.H.,

A Villalon D.K., Murny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

A Villalon D.K., Murny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

A William A., Youchman J.W., Schwutz J., Myers R.M.,

A Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

B Batesiley R.W., Touchman J.W., Green E.D., Dickson M.C.,

B Batesiley S.M., Krzywinski M.I., Skalaka U., Smailus D.E.,

A Schnerch A., Schein J.B., Jones S.J.M., Marra M.A.;

A Robertation and initial analysis of more than 15,000 full-length

Phuman and mouse cDNA sequences.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-077-1996 (Rel. 34, Created)
01-077-1996 (Rel. 34, Last sequence update)
15-MRA-2004 (Rel. 43, Last annotation update)
Transcription factor MafB (V-maf musculoaponeurotic fibrosarcoma oncogene homolog B) (Transcription factor MARI) (Segmentation protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "The mouse segmentation gene kr encodes a novel basic domain-leucine zipper transcription factor."; cell 79:1025-1034(1994).
                                                                                                                                                                                                                                                                                                                                                             Gaps
       GO, GO: 0005634; C:nucleus; TAS.
GO; GO: 0007423; P: sensory organ development; TAS.
InterPro; IPR004821; FE bill.
InterPro; IPR004826; TF Maf.
InterPro; IPR004826; TF Maf.
Pfam; PF03131; bill Maf.
PROSITE; PS50217; Bill 1.
PROSITE; PS50217; Bill 1.
PROSITE; PS50036; Bill 2.
PROSITE; PS00036; Bill 2.
Iranscription regulation; Repressor; DNA-binding; Nuclear protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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Q -> H (IN REF. 1).
AOF3C09F8936CB16 CRC64;
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                                                                                                                                                                                                    LEUCINE-ZIPPER.
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0; Mismatches
                                                                                                                                                                                     BASIC MOTIF
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MEDLINE=95094266; PubMed=8001130;
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                                                                                                                                                                                                                                                                                                                            62.5%;
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STRAIN=FVB/N; TISSUE=Liver;
                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 75.0
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
                                                                                                                                                                                                                        143
                                                                                                                                                                                                                                                          52
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KR) (Kreisler).
MAFB OR MAF1 OR KRML.
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                                                                                                                                                                                                                      131
158
158
12
22
323 AA;
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                                                                                                                                                                                       DNA BIND
                                                                                                                                                                                                                                                            CONFLICT
                                                                                                                                                                                                                                                                                               SEQUENCE
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                                                                                                                                                                                                         DOMAIN
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MAFB MOUSE
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maf related genes: specific expression in chondrocytes, lens and
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16-OCT-2001 (Rel. 40, Last seqn
16-OCT-2001 (Rel. 40, Last anno
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                                                                 spinal cord.";
Oncogene 14:745-750(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 75.0.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
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V181_FOWE.
ID V181_FOWE.
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V181 FOWPV
                          RAH TARAH TA
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GO; GO:0000537; P:DNA binding; IDA.
GO; GO:0007379; P:Segment specification; IMP.
InterPro; IPR008917; Euk transcr_DNA.
InterPro; IPR004827; TF_EZIP.
InterPro; IPR004826; TF_Maf.
FF09131; bZIP Maf; 1.
SMART; SM00338; BRLZ; 1.
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
-!- FUNCTION: Plays a pivotal role in regulating lineage-specific hematopoidesis by repressing ETS1-mediated transcription of erythroid-specific gene in myeloid cells.
-!- SUBCELLULAR LOCATION: Nuclear.
-!- TISSUE SPECIFICITY: MOST ABUNDANT IN KIDNEY, GUT, LUNG, AND BRAIN.
-!- DEVELOPMENTAL STAGE: DETECTABLE AT 8.0 DPC (ONE SOMITES) AS A BAND IN THE CAUDAL HINDBRAIN, AND BY 8.5 DPC (SIX TO EIGHT SOMITES), THE HIGH LEVEL DOMAIN EXHIBITS A SHARP ROSTRAL EDGE COINCIDENT WITH THE R4/R5 BOUNDARY AND A DIFFUSE CAUDAL EDGE LOCATED MIDWAY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI_TaxID=10116;
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N->S: LOSS OF TRANSCRIPTIONAL ACTIVITY.
D77AE07AE09C2AD2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Transcription regulation; Repressor; DNA-binding; Nuclear protein.
DNA BIND 238 264 BASIC MOTIF.
DONAIN 266 287 LEUCINE-ZIPPER.
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28-FEB-2003 (Rel. 41, Last annotation update)
Transcription factor MafB (V-maf musculoaponeurotic fibrosarcoma oncogene homolog B) (Transcription factor MAFI).
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STRAIN-Wistar; TISSUE-Liver;
MEDLINE-97190228; PubMed=903833;
Sakai M., Imaki J., Yoshida K., Ogata A., Matsushima-Hibaya Y.,
Kuboki Y., Nishizawa M., Nishi S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .;
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Pred. No. 43;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; L36435; AAA65689.1; -.
EMBL; BC038256; AAH38256.1; -.
PIR; L95529; L49529.
TRANGFAC; T01439; -.
MGD; MGI:104555; Mafb.
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01-0CT-1996 (Rel. 34, Last seq
28-FEB-2003 (Rel. 41, Last ann
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MAFB RAT
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                       Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
-!- FUNCTION: Plays a pivotal role in regulating lineage-specific hematopoiesis by repressing ETS1-mediated transcription of erythroid-specific genes in myeloid cells (By similarity). -!- SUBCELLULAR LOCATION: Nuclear. -!- SIMILARITY: Belongs to the bZIP family. Maf subfamily.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=20193820; PubMed=10729156; Afonso C.L., Tulman B.R., Lu Z., Zsak L., Kutish G.F., Rock D.L.; The genome of fowlpox virus."; The genome of fowlpox virus."; J. Virol. 74:3815-3831(2000).
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Last annotation update)
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Pred. No. 43;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SPECISE=M.tuberculosis, STRAIN=H37Rv;
MEDLINE=89295987; PubMed=9634230;
MEDLINE=89295987; PubMed=9634230;
Gordon S.V., Espeneier K., Barkhill J., Barry C.E. III, Tekaia F.,
Badcock K., Basham D., Brown D., Chillingworth T., Connor R.,
Badcock K., Basham D., Brown D., Chillingworth T., Connor R.,
Badcock K., Basham D., Brown D., Chillingworth T., Connor R.,
Hornsby T., Jagels K., Kroph A., McLean J., Moule S., Mumphy L.,
Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J.,
Sulston J.E., Taylor K., Whitchhead S., Squares R.,
"Deciphering the biology of Mycobacterium tuberculosis from the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SPECIES—M. tuberculosis, STRAIN-CDC 1551 / Oshkosh,
MEDLINE=22206494; PubMed=12218036;
Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,
Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,
Kolonay J.F., DeBoy R., Dodson R., Gwinn M., Haft D., Hickey E.,
Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M., Salzberg S.L.,
Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula A.,
Bishai W., Jacobs W.R. Jr., Venter J.C., Fraser C.M.;
"Whole-genome comparison of Mycobacterium tuberculosis clinical and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PERCIES. M. Dovis, N. S. TRAIN=AF2122/97;

MEDLINE=22709107; PubMed=12788972;

Garnier T., Eiglmeier K., Camus J.-C., Medina N., Mansoor H.,

Garnier T., Eiglmeier K., Camus J.-C., Medina N., Mansoor H.,

Bryor M., Duthoy S., Grondin S., Lacroix C., Monsempe C., Simon S.,

Harris B., Atkin R., Doggett J., Mayes R., Keating L., Wheeler P.R.,

Parkhill J., Barrell B.G., Cole S.T., Gordon S.V., Hewinson R.G.;

"The complete genome sequence of Mycobacterium bovis.";

Proc. Natl. Acad. Sci. U.S.A. 100:7877-7882(2003).

-!- SIMILARITY: Belongs to the ATP-dependent AMP-binding enzyme
                                                                                                   Gaps
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0
                                                                                                                                                                                                                                                                                                                    16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Putative fatty-acid--CoA ligase fadD21 (EC 6.2.1.-) (Acyl-CoA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Mycobacteriaceae; Mycobacterium.
NCBI_TaxID=1773, 1765;
                                                          DB 1; Length 369;
50;
                      369 AA; 42081 MW; 380A71032C18BB99 CRC64;
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                                                                                                                                                                                                                                                                                    578 AA.
                                                                                                     2; Mismatches
                                                            62.5%; Score 35;
50.0%; Pred. No. E
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                                                                                                                                                                                                                                                                                                                                                                                                                                              Mycobacterium tuberculosis, and Mycobacterium bovis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            complete genome sequence.";
Nature 393:537-544(1998).
      Pfam; PF03003; DUF230; 1.
                                                                                 Best Local Similarity 50.0
Matches 5; Conservative
                                                                                                                                                                                                                                                                                    STANDARD;
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                                                                                                                                             1 CISVPLSVPC 10
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(c) 1993 - 2004 Compugen Ltd.
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5, 2004, 09:46:09; Search time 22.6263 Seconds (without alignments) 139.448 Million cell updates/sec September Run on:

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BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

1017041 seqs, 315518202 residues Searched:

1017041 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

SPTREMBL_25:*
1: Sp archea:*
2: Sp_bacteria:*
3: Sp fung1:*
4: Sp_human:*
5: Sp_invertebrate:*
5: Sp_mammal:*
6: Sp_mammal:*
6: Sp_mhc:*
7: Sp_mammal:*
7: Sp_mhc:*
8: Sp_organelle:*
8: Sp_organelle:*
8: Sp_organelle:*
8: Sp_organelle:*
8: Sp_organelle:*
8: Sp_organelle:*
8: Sp_organelle:* sp_rodent:* sp_plant:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

unclassified:*

sp archeap:*

sp vertebrate: * rvirus:* _bacteriap:*

virus:*

STIMMARTES

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66.1 66.1 66.1 66.1 66.1	64.3 64.3 64.3	64.3 64.3 64.3	4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4	62.5 62.5 62.5 62.5	62.5 62.5 62.5 62.5 62.5
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11 20 21 22	22 24 25 25	27 28 30	2 2 2 2 2 4 2 5 4 5 5 5 5 5 5 5 5 5 5 5	333 433 40 40	41 44 45

ALIGNMENTS

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STRAIN-TU 2353;

MEDLINE-21225632; PubWed=11325225;

Rafanan E.R. Jr., Le L., Zhao L., Decker H., Shen B.;

Rafanan E.R. Jr., Le L., Zhao L., Decker H., Shen B.;

"Cloning, sequencing, and heterologous expression of the elmGHIJ genes involved in the biosynthesis of the polyketide antibiotic elloramycin from Streptomyces ollvaceus Tu2353.";

J. Nat. Prod. 64:444.449(2011).

EMBL; AF263463; AAF73051.1;

GO; GO:0004497; F:monooxygenase activity; IEA.

InterPro; IPR007138; ABM.
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                                                                                                                                         Streptomyces olivaceus.
Bacteria, Actinobacteridae, Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.
NCBI_TaxID=47716;
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                                                                                                                                                                                                                                                                                                                                                                                                                                         109 AA; 12304 MW; E65F4010C7D4B30B CRC64;
                                                            01-0CT-2000 (TrEMBLrel. 15, Created)
01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-0UN-2003 (TrEMBLrel. 24, Last annotation update)
                                    109 A.A.
                                   PRT;
                               PRELIMINARY;
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les 7; Conservative
                                                                                                              Tcm F1 monooxygenase.
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                                 Q9L4Y0
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RESULT 1
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Local Similarity 66.7
nes 6; Conservative
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                                                                                                                                                                                                                                                                                      27 VEVPLAVPC
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STRAIN=ATCC 15692 / PAO1;
MEDLINE=20437337; PubMed=10984043;
MEDLINE=20437337; PubMed=10984043;
Stover C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warrener P.,
Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M.,
Garber R.L., Goltry L., Tolentino E., Westbrock Wadman S., Yuan Y.,
Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M.,
Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,
Reizer J., Saier M.H., Hancock R.E.W., Lory S., Olson M.V.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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"The R-type pyocin of Pseudomonas aeruginosa is related to P2 phage, and the F-type is related to lambda phage.";
Mol. Microbiol. 38:213-231(2000).

EMBL; AB030826; BAA83139.1; -.
InterPro; IPR000437; Prok lipoprot S.
Hypothetical protein.

SEQUENCE 85 AA; 9252 MW; 472269231FCCG355 CRC64;
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STRAIN=ATCC 15692 / PAO1;
Nakayama K., Takashima K., Ishihara H., Shinomiya T., Kageyama M., Kanaya S., Ohnishi M., Murata T., Terawaki Y., Mori H., Hayashi T.;
"Genatic relationship between bacteriochns and bacteriophages.";
Submitted (AUG-1999) to the EMBL/GenBank/DDBJ databases.
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                                                                                                                               Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
                                                                                 Last annotation update)
                                                                    Last sequence update)
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Pred. No. 8.8;
2; Mismatches
                 85 AA
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                 PRT;
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Best Local Similarity 66.7
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27 VEVPLAVPC 35
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01-OCT-2003
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MEDLINEE-1995/17; Fubmed=10910340.

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A lavarenga R., Alves L.M.C., Arraya J.E., Baia G.S., Baptista C.S.,
A larros M.H., Bonaccorsis E.D., Bordin S., Bove U.M., Briones M.R.S.,
Buenco M.R.P., Camargo A.A., Camargo L.E.A., Carraro D.M., Carrer H.,
Colauto N.B., Colombo C., Costa F.F., Costa M.C.R., Costa Neto C.M.,
Colauto D.E., Cristofani M., Dias-Neto E.D., Docena C., El-Dorry H.,
R. Coldman G.D., Franca S.C., Franco M.C., Frome M., Furlan L.R.,
A ranga J.S., Franca S.C., Franco M.C., Frome M., Furlan L.R.,
A darnier M., Goldman M.H., Kemper E.L., Kitajima J.P.,
A Krieger J.E., Kuramae E.E., Laigret F., Lambais M.R., Leite L.C.C.,
A Machado M.A., Madeira A.M.B.W., Madeira H.M.F., Marino C.L.,
A Machado M.A., Madeira A.M.B.W., Madeira H.M.F., Marino C.L.,
A Mannako M. Mariacas B.C., Miyaki C.Y., Monteiro-Vitorello C.B.,
Mond D.H., Nagai M.A., Nascimento A.L.T.O., Netto L.E.S.,
Nani A. Jr., Nobrega F.G., Nunes L.R., Oliveira M.A.,
A de Souza W.B., Trans G.A.G., Rodrigues V., de Rosa A.J. M.,
A de Souza A.B., Roberto P.G., Rodrigues V., de Rosa A.J. M.,
A da Silva A.C.R., da Silva F.R., Silva W.A., Jr.,
A da Silva A.C.R., Silvestri M.L.Z., Siqueira W.J., de Souza A.A.,
Nallada H., Van Sluys M.A., Verjovski-Almeida S., Vettore A.L.,
The genome sequence of the plant pathogen Xylella fastidiosa.";
The genome sequence of the plant pathogen Xylella fastidiosa.";
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Xanthomonadaceae; Xylella.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 69.6%; Score 39; DB 16; Length 85; 66.7%; Pred. No. 8.8; 1; Indels ive 2; Mismatches 1; Indels
"Complete genome sequence of Pseudomonas aeruginosa PAO1, opportunistic pathogen.";
Nature 406:959-964 [2000).
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148 AA; 15990 MW; B78D2FAB6B929260 CRC64;
                                                                                                                   EMBL; AB030825; BAA83170.1; -.
EMBL; AB045308; BAA9749.1; -.
EMBL; AB04498; AAG04020.1; -.
EMBL; AE004498; AAG04020.1; -.
InterPro; IPR000437; Prok lipoprot S.
PROSTTE; PS00013; PROKR LIPOPROTETIN; 1.
Hypochetical protein; Complete proteome:
SEQUENCE 85 AA; 9222 MM; F2267D9C5427748 CRC64;
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01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Hypothetical protein Xf2118.
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EMBL; AE004026; AAF84917.1; -.
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SEQUENCE
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MEDLINE=91333007; PubMed=1651403;
Teo I.A., Griffin B.E., Jones M.D.;
"Characterization of the DNA polymerase gene of human herpesvirus 6.";
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Gompels U.A., Nicholas J., Lawrence G., Jones M., Thomson B.J.,
Martin M.E., Efstathiou S., Craxton M., Macaulay H.A.;
"The DNA sequence of human herpesvirus-6: structure, coding content,
     Gaps
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J. Virol. 64:287-299(1990),
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Lawrence G.L., Chee M., Craxton M.A., Gompels U.A., Honess R.W.,
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Thomson B.J., Efstathiou S., Honess R.W.;
"Acquisition of the human adeno-associated virus type-2 rep
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Chang C.K., Balachandran N.; "Identification, characterization, and sequence analysis encoding a phosphoprotein of human herpesvirus 6."; J. Virol. 65:2884-2894(1991).
     Indels
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MEDLINE-92333249; PubMed=1321206;
Efstathiou S., Lawrence G.L., Brown C.M., Barrell B.G.;
                                                                                                                                                                                                                                                                                                     RNA stage; Herpesviridae;
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Last annotation update)
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                                                                                                                                                            620 AA.
 Mismatches
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MEDLINE=91237802; PubMed=1851860;
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25,
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Nature 351:78-80(1991).
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5; Conservative
                                                                                                                                                          PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                and genome evolution.";
Virology 209:29-51(1995)
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                                                                                                                                                                                                                                                                                                 Viruses; dsDNA viruses,
                                 CISVPLSVPC 10
                                                                    CCAVPMNAPC 17
                                                                                                                                                                                                                                            Hypothetical protein.
DR2.
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SEQUENCE FROM N.A.
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01-OCT-2003
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Matches
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08983

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AC 08988

DD 1-NO
DD 01-NO
DD 01-NO
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Thomson B.J., Honess R.W.; The right end of the unique region of the genome of human herpesvirus of 1102 contains a candidate immediate early gene enhancer and a homologue of the human cytomegalovirus US22 gene family."; J. Gen. Virol. 73:1649-1660(1992).
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"Identification of homologues to the human cytomegalovirus US22 gene family in human herpesvirus 6.1, J. Gen. Virol. 73:1661-1671(1992).
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MEDLINE=9405558; PubMed=7692666;
Liu D.K., Gompels U.A., Foa-Tomasi L., Campadelli-Fiume G.;
Liu n.K., Gompels U.A., Foa-Tomasi L., Campadelli-Fiume G.;
"Human herpesvirus-6 glycoprotein H and L homologs are components of the gpl00 complex and the gH external domain is the target for neutralizing monoclonal antibodies.";
                                                                                                                                                                                                                          Geng Y., Chandran B., Josephs S.F., Wood C.; "Identification and characterization of a human herpesvirus 6 gene segment that trans activates the human immunodeficiency virus type
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Neipel F., Ellinger K., Fleckenstein B.;
"Gene for the major antigenic structural protein (p100) of human
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "The glycoprotein B homologue of human herpesvirus 6.";
J. Gen. Virol. 74:495-500(1993).
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MEDLINE=93091236; PubMed=1333836;
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MEDLINE=92260671; PubMed=1374813;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     marrow transplant patients."; J. Gen. Virol. 74:613-622(1993).
                                                                                                                                                                                                                                                                                                                                                           Virol. 66:1564-1570(1992)
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STRAIN=U1102;
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Last sequence update)
Last annotation update)

Created)

144 AA.

PRT;

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Saccharomyces cerevisiae (Baker's yeast).
Bukaryota, Fungi, Ascomycota, Saccharomycotina, Saccharomycetes;
Saccharomycetales, Saccharomycetaceae, Saccharomyces.
                                                                                     (TrEMBLrel. 21, (TrEMBLrel. 21, (TrEMBLrel. 25,
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                                                                                                                                                      Hypothetical protein.
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RESULT 6
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                       MEDINE=93331710; PubMed=7687803; Pellett P., Sanchez-Martinez D., Dominguez G., Black J.B., Anton E., Greenamoyer C., Dambaugh T.R., A strongly immuncactive virion protein of human herpesvirus 6 variant B errain Z29: identification and characterization of the gene and mapping of a variant-specific monoclonal antibody reactive
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Nicholas J., Martin M.;
Nicholas J., Martin M.;
"Nucleotide sequence analysis of a 38.5-kilobase-pair region of the genome of human herpesvirus 6 encoding human cytomegalovirus immediate early gene homologs and transactivating functions.";
J. Virol. 68:597-610(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Dewhurst S., Dollard S.C., Pellett P.E., Dambaugh T.R.; "Identification of a lytic-phase origin of DNA replication in human herpesvirus 6B strain Z29."; J. Virol. 67:7680-7683(1993).
                                                                                                                                                                                                                                                                                                                                 "Identification and mapping of the gene encoding the glycoprotein complex gp82-gp105 of human herpesvirus 6 and mapping of the neutralizing epitope recognized by monoclonal antibodies."; J. Virol. 67:4611-4620(1993).
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Thompson J., Choudhury S., Kashanchi F., Doniger J., Berneman Z.,
Frenkel N., Rosenthal L.J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gompels U.A., Macaulay H.A.; "Characterization of human telomeric repeat sequences from human herpesvirus 6 and relationship to replication."; Gen. Virol. 76:451-458(1995).
                                                                                                                                                                                                                                                                       MEDLINE-93323202; PubMed-7687301;
Pfeiffer B., Berneman Z.N., Neipel F., Chang C.K., Tirwatnapong
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MEDLINE=94047392; PubMed=8230490;
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J. Virol. 68:2978-2985(1994).
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Best Local Similarity 77.8
Matches 7; Conservative
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Gaps
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01-0CT-2002 (TrEMBLrel. 22, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
11-0CT-2003 (TrEMBLrel. 25, Last annotation update)
11-0CT-2003 (TrEMBLrel. 25, Last annotation update)
Arabidopsis thaliana (Mouse-ear cress).
Arabidopsis thaliana (Mouse-ear cress).
Bukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; Spermatophyta; Magnoliophyta; Brassicaceae; Arabidopsis.
SEQUENCE FROM N.A.

MEDLINE=21624570; PubMed=11753363;

MEDLINE=21624570; PubMed=11753363;

Minar A., Harrison P.M., Cheung K.H., Lan N., Echols N., Bertone I.

Miller P., Gerstein M.B., Snqder M.;

"An integrated approach for finding overlooked genes in yeast.";

"An integrated approach for finding overlooked genes in yeast.";

MAL. Biotechnol. 20:58-63(2002).

Hypothetical protein.

SEQUENCE 144 AA; 16381 MW; 43F0BFCF4F5B1BFA CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 503;
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TIGRFAMs; TIGN01302; 1.
PROSITE; PS00487; IMP DH GMP RED; 1.
SEQUENCE 503 AA; 54218 MW; 99D478F48F4E649C CRC64;
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73;
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                                                                                                                                                                                                                                                                                                                                                                                                                          503 AA.
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Pred. No.
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85.7%;
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Best Local Similarity 75.v.
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Best Local Similarity
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Gaps

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Indels

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Gilakjan Z.A., Kropinski A.M.; "Coning and analysis of the capsid morphogenesis genes of Pseudomonas aeruginosa bacteriophage 13: another example of protein chain mail?"; J. Bacteriol. 181:7221-7227(1999).
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Viruses; dsDNA viruses, no RNA stage; Caudovirales; Siphoviridae;
Lambda-like viruses.
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Xanthomonadaceae; Xylella.
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J. Bacteriol. 18:2666-6074 (2000).

EMBL; AFI65214; AAF80793.1; -.
InterPro: IPROGNAT; Prok lipoprot S.
PROSITE; PS00013; PROKAR LIPOPROTEIN; 1.
SEQUENCE 86 AA; 9389 MM; 86ABCAB2B2A9ES9F CRC64;
                                                                                                                                                                                                                                                               67.9%; Score 38; DB 16; Length 563; 60.0%; Pred. No. 81;
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Pred. No. 21;
3; Mismatches 1; Indels
       GO; GO:0000034; F:adenine deaminase activity; IEA.
GO; GO:0016787; F:hydrolase activity; IEA.
InterPro; IPR06680; Amidohydro_1.
Pfam; PF01979; Amidohydro_1; 1.
Hydrolase; Complete proteome.
SEQUENCE 563 AA; 60927 MW; A4B5159C11718FA7 CRC64;
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55.68;
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XF2736.
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Best Local Similarity 60.00,
Pest 6, Conservative
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28 VEVPIAVPC 36
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SEQUENCE FROM N.A.
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MEDLINE=22884998; PubMed=12597275;
Kaneko T., Nakamura Y., Sato S., Minamisawa K., Uchiumi T.,
Sasamoto S., Watanabe A., Idesawa K., Iriguchi M., Kawashima K.,
Kohara M., Matsumoto M., Shimpo S., Tsuruoka H., Wada T., Yamada M.,
Tabata S.;
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MEDLINE=22480296; PubMed=1256566;
Kleerebezem M., Boekhorst J., van Kranenburg R., Molenaar D.,
Klupers O.P., Leer R., Tarchini R., Peters S.A., Sandbrink H.M.,
Fiers M.W.E.J., Stiekema W., Klein Lankhorst R.M., Bron P.A.,
Hoffer S.M., Nierop Groot M.N., Kerkhoven R., De Vries M., Ursing Be Vos W.M., Siezen R.J.;
"Complete genome sequence of Lactobacillus plantarum WCFS1.";
Proc. Natl. Acad. Sci. U.S.A. 100:1990-1995(2003).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Complete genomic sequence of nitrogen-fixing symbiotic bacterium Bradyrhizobium japonicum USDA110.";
DNA Res. 9:189-197(2002).
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Bradyrhizobiacea; Bradyrhizobium.
NCBI_TaxID=375;
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       0; Indels
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Lactobacillus,
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Last annotation update)
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01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Adenina deaminase (EC 3.5.4.2).
ADEC OR LP 3334.
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InterPro; IPR002830; carboxylyase.
InterPro; IPR000585; Hemopexin.
       1;
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PROSITE; PS00024; HEMOPEXIN; 1.
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   6; Conservative
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Best Local Similarity 66.7
Matches 6, Conservative
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284 CLTVPLEVP 292
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SEQUENCE 528 AA;
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SEQUENCE FROM N.A.
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              Simpson A.J.G., Reinach F.C., Araya J.E., Baia G.S., Baptista C.S.,
Alvarenga R., Alves L.M.C., Araya J.E., Baia G.S., Baptista C.S.,
Alvarenga R.H., Bonaccorsi E.D., Bordin S., Bove J.M., Briones M.R.S.,
Bueno M.H., Bonaccorsi E.D., Bordin S., Bove J.M., Briones M.R.S.,
Bueno M.H., Colombo C., Costa F.F., Costa M.C.R., Carraro D.M., Carrer H.,
Colauto N.B., Colombo C., Costa F.F., Costa M.C.R., Costa-Neto C.M.,
A colinho L.L., Cristofani M., Dias-Neto E., Docena C., El-Dorry H.,
Radinan A.D., Ferreira A.J.S., Ferreira V.C.A., Ferro J.A.,
Rraga J.S., Franca S.C., Franco M.C., Frohme M., Futlan L.R.,
A Fraga J.S., Kuramae E.E., Laigret F., Lambais M.R., Leite L.C.C.,
Lemos E.G.M., Lemos M.V.F., Lopes S.A., Lopes C.R., Machado J.A.,
Machado M.A., Madeira A.M.B.N., Madeira H.M.F., Marino C.L.,
Marques M.V., Martins E.A.L., Martino C.L.,
Marques M.V., Martins E.A.L., Martino C.L.,
Mandol M.A., Madeira A.M.B.N., Materins M.P., Paris A.,
Moch C.F.M., Miracca E.C., Niyaki C.Y., Monteiro-Vitorello C.B.,
Moon D.H., Nagaim M.A., Nascimento A.L.T.O., Netto L.E.S.,
Moon D.H., Nagaim M.A., Nascimento A.L.T.O., Netto L.E.S.,
Mannia A. Jr., Nobrega F.G., Nunes L.R., Oliveira M.A.,
A de Silva A.C., de Sa R.G., Santelli R.V., Sawasaki H.E.,
A da Silva A.C.R., da Silva A.M., da Silva F.R., Silva M.A. Ju.,
A de Souza A.P., Terenzi M.F., Truffi D., Tsai S.M., Tsuhako M.H.,
A dago M.A., Zatz M., Maidains W.J., Setuball J.C.,
A dago M.A., Zatz M., Waldains W.J., Setuball J.C.,
A dago M.A., Zatz M., Waldains W.J., Setuball J.C.,
A dago M.A., Zatz M., Waldains W.J., Setuball J.C.,
A dago M.A., Zatz M., Waldains W.J., Setuball J.C.,
A dago M.A., Zatz M., Waldains W.J., Setuball J.C.,
A dago M.A., Zatz M., Waldains W.J., Setuball J.C.,
A dago M.A., Zatz M., Waldains W.J., Setuball J.C.,
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the RIKEN Genome Exploration Research Group Phase I & II Team;
the RIKEN Genome Exploration Research Group Phase I & II Team;
the RIKEN Genome Exploration Research Group Phase I & II Team;
handlysis of the mouse transcriptome based on functional annotation of
60,770 full-length cDNAs.;
Nature 420:563-573 (2002).
BMBL: AKO53082; BAC35260.1; -.
Hypothetical protein.
SEQUENCE 129 AA; 13584 MW; DOBB3B75AFAD595B CRC64;
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "The genome sequence of the plant pathogen Xylella fastidiosa.";
Nature 406:151-159(2000).
BMBL; AB004080; AAR85521.1; -.
PIR; F82521; F82521.
Hypothetical protein; Complete proteome.
SEQUENCE 89 AA; 9641 MW; F13175F1054D6130 CRC64;
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01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Hypothetical sugar phosphatases structure containing protein.
Mus musculus (Mouse).
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STRAIN=C57BL/6J; TISSUE=Head;
MEDLINE=22354683; PubMed=12466851;
          MEDLINE=20365717; PubMed=10910347;
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Best Local Similarity
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BMBL, AROPITOI, BACOS145.1; -.

Hypothetical protein.

SEQUENCE 134 AA; 14294 MW; 06EA299087CBC41F CRC64;
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                                                                                                                                                          Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nakamura Y., Kaneko T., Sato S., Ikeuchi M., Katoh H., Sasamoto & Watanabe A., Iriguchi M., Kawashima K., Kimura T., Kishida Y., Kiyokawa C., Kohara M., Matsumoto M., Matsuno A., Nakazaki N., Shimpo S., Sugimoto M., Takeuchi C., Yamada M., Tabata S.; "Complete genome structure of the thermophilic cyanobacterium Thermosynechococcus elongatus BP-1."; pnA Res. 9:123-130(2002).

EMBL; AP005369; BAC07619.1; -. Complete proteome.

SEQUENCE 155 AA; 17833 MW; 16CDEP9F696CEC331 CRC64;
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Bacteria; Cyanobacteria; Chrococccales; Synechococcus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                          01-OCT-2002 (TrEMBLrel. 22, Last sequence update) 01-OCT-2002 (TrEMBLrel. 22, Last annotation update) Hypothetical protein FLJ40382.
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Last annotation update)
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Pred. No. 37;
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134 AA
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MEDLINE=22225144; PubMed=12240834;
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                                                  01-OCT-2002 (TrEMBLrel. 22,
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Best Local Similarity 77.8
Matches 7; Conservative
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PRELIMINARY;
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46 CIAGPLLLPC
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Best Local Similarity
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NCBI_TaxID=32046;
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94 CQSLPLSVP 102

Search completed: September 5, 2004, 10:00:07 Job time: 24.6263 secs

1 CISVPLSV 8 | :|:|||: | | : | 39 CVSIPLSI 46

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GenCore version 5.1.6
(c) 1993 - 2004 Compugen Ltd.
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September 5, 2004, 09:37:49 ; Search time 32.8283 Seconds	(without alignments)	86.068 Million cell updates/sec
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Title:	US-09-761-636A-13
Perfect score:	56
Sequence:	1 CISVPLSVPC 10

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

1586107 seqs, 282547505 residues Searched:

1586107 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

geneseqp1980s:*
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geneseqp2000s:*
geneseqp2001s:* A_Geneseq_29Jan04:* 1: genesedr1980... geneseqp2002s:* geneseqp2003as:* geneseqp2003bs:* geneseqp2004s:* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

			Description		Aau04532 VEGF 1	Aan04526 VEGE 1	107
SUMMARIES			ID		10 4 AAU04532	AAU04526	
			DB	-	4	4	•
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Description	Aau04532 VEGF base	6 VEGF has	4 Human	42 VEGF b		5 VEGF		4 Human	6 Human	7 Human	8 Human	3 VEGF b	2 Novel	0 Novel	3 Peptic		0	4	8 Arabid	σ.	m	0	80	- T	Abbesess Drosophil
ID	AAU04532	AAU04526	AAR66394	AAU04542	AAU04533	AAU04545	AAU04544	AAM95534	ABB96216	AAM95827	ABB96358	AAU04543	ABG12542	ABG12530	AAM16003	ABB20407	ABG37710	ADB64084	AAG30888	AAG20989	AAG43108	ABB15040	ABB67498	ABG21894	ABB65635
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% Query Match	100	8	80	77	74	74	72	69	69	69	69	9	67	67	67	63					67	99	99	99	99
Score	99	45.5	4	43.5	41.5	41.5	40.5	39	39		.39	38.5	38	38	38	38	38	38						37	37
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ABG20151 ABG71244 AAR96138 AAW82212 AAW46562 AAW18478 ABW54997 ABP64007 AAB45459	AAB45460 AAG89148 AAG85461 ABG19452 ABG6053 AAG6053 AAG04076 AAM79027 AAM80011	
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ALIGNMENTS

RESULT 1

AAU04532 standard; peptide; 10 AA. VEGF based monocyclic peptide 10. (first entry) 26-SEP-2001 AAU04532; AAU04532

Human; VEGF; vascular endothelial growth factor; angiogenesis; neovascularisation; lymphangiogenesis; psoriasis; tumour; diabetes induced neovascular sequelae; rheumatoid arthritis; diabetic retinopathy; chronic inflammation; cyclic.

Synthetic.

1. .10 /note= "This bond cyclises the peptide" Location/Qualifiers 18-JAN-2000; 2000US-0176293P. L8-JAN-2001; 2001WO-US001533. Key Disulfide-bond WO200152875-A1. 26-JUL-2001.

(LUDW-) LUDWIG INST CANCER RES.

Stacker S, Hughes RA, WPI; 2001-442248/47. Achen MG,

Cendron A;

Novel monomeric monocyclic peptide, used to interfere with angiogenesis, or lymphangiogenesis, is produced by cyclizing a peptide loop fragment from an exposed loop of a growth factor protein by oxidizing the cysteine residues.

Claim 49; Page 32; 102pp; English.

The sequence represents a monomeric monocyclic peptide of the invention, whose 3-dimensional structure is modelled on the expose loop of human VEGFD (vascular endothelial growth factor). The invention relates to a method of producing a monomeric monocyclic peptide by a measuring betabeta carbon separation distances on opposite antiparallel strands of a

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peptide loop fragment from an exposed loop of a growth factor protein and cyclising the peptide by oxidising the cysteine residues. The monocyclic peptides and a cyclic peptides (comprising 2 linked monocyclic peptides) and a cyclic peptide with at least one amino acid deleted prior to cyclisation are used to interfere with anglogenesis.

Co neovascularisation or lymphangiogenesis in a mammal with a condition characterised by anglogenesis, neovascularisation or lymphangiogenesis.

Co receptoracy ascularised malignant or benigh tumour, post-recovery cerebrovascular accident, post-angloplasty restenosis, heat or cold trauma, substance-induced neovascularisation of the liver, excessive crevenone-related anglogenic dysfunction, diabetes induced neovascular certained naplogenic diabetes induced neovascular permeability in a mammal (the mammal has a condition characterised by fluid cavity, pleura, or brain. The peptides are used to induced neovascular used to interfere with at least one biological activity induced by VEGF, VEGF-C or D and are also used in combination with an anti-inflammatory agent, to treat a chronic inflammation, with an anti-inflammatory agent, to treat a chronic inflammation with an anti-inflammatory agent, to treat a chronic inflammation with an anti-inflammatory agent, to treat a chronic inflammatory agent, to treat a continual process of the continual process of the continual process of the continual process of the continual process of t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       neovascularisation, lymphangiogenesis; psoriasis; tumour; diabetes induced neovascular sequelae; rheumatoid arthritis; diabetic retinopathy; chronic inflammation; cyclic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%; Score 56; DB 4; Length 10; 100.0%; Pred. No. 0.0098; ive 0; Mismatches 0; Indels

    .11
    /note= "This bond cyclises the peptide"

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             diabetic retinopathy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 10 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAU04526;
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The sequence represents a monomeric monocyclic peptide of the invention, whose 3-dimensional structure is medelled on the expose loop of human C VEGPD (vascular endothelial growth factor). The invention relates to a method of producing a monomeric monocyclic peptide by a measuring betact carbon separation distances on opposite antiparallel strands of a peptide loop fragment from an exposed loop of a growth factor protein and cyclising the peptide by oxidising the cysteine residues. The monocyclic peptides, dimeric bicyclic peptides (comprising 2 linked monocyclic peptides) and a cyclic peptide with at least one amino acid deleted prior to cyclisation are used to interfere with angiogenesis, condition are used to interfere with angiogenesis, or neovascularisation or lymphangiogenesis, neovascularisation or lymphangiogenesis. The condition is diabetic retinopathy, psoriasis, arthropathy.

The condition is diabetic retinopathy, psoriasis, arthropathy.

C cerebrovascular accident, post-angioplasty restenosis, head, heat or crauma, substance-induced neovascularisation of the liver, excessive trauma, substance-induced neovascularisation of the liver, excessive corpresent angiogenic dysfunction, diabetes induced neovascular sequelae, hypertension induced neovascular sequelae, or chronic liver infection. The peptides are also used to modulate vascular permeability or brain. The peptides are used to image blood vessels and lymphatic vasculature. The monomeric and bicyclic peptides are used to interfere covery curulation in peripheral limbs or in lungs, peritoneal cavity, to treat a compliation with at least one biological activity induced by VEGF-C or -D and continon inflammation, especially rheumatoid arthritis, psoriasis and diabetic retinorathy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1,
                                                                      sequence represents a monomeric monocyclic peptide of the invention,
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/note= "X corresp. to translated stop codon"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 45.5; DB
Pred. No. 0.56;
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAR66394 standard; peptide; 141 AA.
                                     Claim 49; Page 32; 102pp; English.
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90.9%;
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(first entry)
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Best Local Similarity 90.9
Matches 10; Conservative
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11-AUG-1995
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      aar66394
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Novel monomeric monocyclic peptide, used to interfere with angiogenesis, or lymphangiogenesis, is produced by cyclizing a peptide loop fragment from an exposed loop of a growth factor protein by oxidizing the cysteine
                                                                                                                                                                                                                                                                                                                                                                                                                                                Human; VEGF; vascular endothelial growth factor; angiogenesis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            neovascularisation, lymphangiogenesis; psoriasis; tumour; diabetes induced neovascular sequelae; rheumatoid arthritis; diabetic retinopathy; chronic inflammation; cyclic.

    .11
/note= "This bond cyclises the peptide"

                                                                                                                                                                                                                                                 80.4%; Score 45; DB 2
77.8%; Pred. No. 9.4;
iive 2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                               AAU04542 standard; peptide; 11 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Stacker S,
                                                                                                                                                                                                                                                                                                                                                                                                                             VEGF based monocyclic peptide 20.
                                                                                Claim 1; Page 56; 87pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (LUDW-) LUDWIG INST CANCER RES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        18-JAN-2001; 2001WO-US001533.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             18-JAN-2000; 2000US-0176293P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        16-MAY-2000; 2000US-0204590P
                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                           Best Local Similarity 77.8
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hughes RA,
                                                                                                                                                                                                                                                                                                     28 CISIPLSIP 36
                                                                                                                                                                                                                                                                                          1 CISVPLSVP 9
          WPI; 1995-006234/01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2001-442248/47.
                   N-PSDB; AAQ75090
                                                                                                                                                                                                                              Sequence 141 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Key
Disulfide-bond
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WO200152875-A1
                                                            schizophrenia
                                                                                                                                                                                                                                                                                                                                                                                                         26-SEP-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    26-JUL-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Achen MG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Synthetic
                                                                                                                                                                                                                                                                                                                                                                                     AAU04542;
                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         residues
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whose 3-dimensional structure is modelled on the expose loop of human CVGFD (vascular endothelial growth factor). The invention relates to a method of producing a monomeric monocyclic peptide by a measuring beta-beta carbon separation distances on opposite antiparallel strands of a peptide loop fragment from an exposed loop of a growth factor protein and cyclising the peptide by oxidising the cysteine residues. The monocyclic peptides dimeric bicyclic peptides (comprising 2 linked monocyclic peptides) and a cyclic peptide with at least one amino acid deleted prior peptides) and a cyclic peptide with at least one amino acid deleted prior cyclistation are used to interfere with angiogenesis, neovascularisation or lymphangiogenesis in mammal with a condition characterised by angiogenesis, neovascularisation or lymphangiogenesis. The condition is diabetic retinopathy, psoriasis, arthropathy, hemangioma, vascularised malignant or benign tumour, post-ecovery cerebrovascular accident, post-angioplasty restenosis, head, heat or cold trauma, substance induced neovascularisation of the liver excessive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    hormone related angiogenic dysfunction, diabetes induced necvascular sequelae, hypertension induced necvascular sequelae, or chronic liver infection. The peptides are also used to modulate vascular permeability in a mammal (the mammal has a condition characterised by fluid accumulation in peripheral limbs or in lungs, peritoneal cavity, pleura, or brain. The peptides are used to image blood vessels and lymphatic vasculature. The monomeric and bicyclic peptides are used to interfere with at least one biological activity induced by VEGF, VEGF-C or -D and are also used in combination with an anti-inflammatory agent, to treat a
                                                                        sequence represents a monomeric monocyclic peptide of the invention,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     inflammation, especially rheumatoid arthritis, psoriasis and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human; VEGF; vascular endothelial growth factor; angiogenesis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              neovascularisation; lymphangiogenesis; psoriasis; tumour; diabetes induced neovascular sequelae; rheumatoid arthritis; diabetic retinopathy; chronic inflammation; cyclic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4; Length 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note= "This bond cyclises the peptide"
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Pred, No. 1.2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
                         Example 25; Page 47; 102pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VEGF based monocyclic peptide 11.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAU04533 standard; peptide; 9 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            77.78;
81.88;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 CISVPL-SVPC 10
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| CLSVPLTSVPC 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               diabetic retinopathy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 11 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Disulfide-bond
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO200152875-A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAU04533;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        chronic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAU04533
ID AAU0
XX
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ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           g
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                                                                                                                                                                                                                                   Psychosis protecting peptide (PP peptide) can be obtd. intitially by using the sequence in AAQ75090 as a basis for designing polymorleotide probes to clone, sequence and express or synthesize PP related proteisn and peptides occurring in normal individuals, and to a substantially lesser degree in individuals with psychotic disorders. The PP encoding gene was discovered using the subtraction cloning of cDNA from manA obtd. from monozygotic twins discordant for schizophrenia and assaying for clones in which expression is greatest in the 'well' twin. A nt sequence substantially corresp. to AAQ7509 is claimed, which comprises 30.X nts, where X=80, 95, 158. 222, 243, 249, 260, 295, 407 or 423. A PP peptide of 10-141 AAs is also claimed. (Updated on 25-MAR-2003 to correct PN field.)
                                                                                     New nucleic acids encoding psychosis protecting peptide and antibodies - for the treatment, diagnosis and research of psychotic disorders, such as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2; Length 141;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Cendron A;
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(LUDW-) LUDWIG INST CANCER RES

18-JAN-2000; 2000US-0176293P. 16-MAY-2000; 2000US-0204590P.

ij

Gaps

26-JUL-2001

Cendron A;

Stacker S,

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Claim 49; Page 32; 102pp; English.
  Achen MG, Hughes RA,
                                                                                        diabetic retinopathy
       WPI; 2001-442248/47.
                   residues
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Sequence 9 AA;

Score 41.5; DB 4; Length 9; Pred. No. 1.4e+06; 0; Mismatches 0; Indels 74.1%; 90.0%; Ouery Match
Best Local Similarity 90.0.
From 9; Conservative 1 CISVPLSVPC 10 σ CISVPL-VPC 셤 à

diabetic retinopathy

Sequence 11 AA;

AAU04545 standard; peptide; 11 AA. AAU04545; RESULT 6 AAU04545

Human; VEGF; vascular endothelial growth factor; angiogenesis; neovascularisation, lymphangiogenesis; psoriasis; tumour; diabetes induced neovascular sequelae; rheumatoid arthritis; diabetic retinopathy; chronic inflammation; cyclic.

/note= "This bond cyclises the peptide" WO200152875-A1

Location/Qualifiers VEGF based monocyclic peptide 23. 26-SEP-2001 (first entry) Disulfide-bond Synthetic

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The Sequence represents a monometric management of the sequence of producting a monometric management of the sequence of producing a monometric monocyclic peptide by a measuring betace the carbon separation distances on opposite antiparallel strands of a peptide loop fragment from an exposed loop of a growth factor protein and cyclising the peptide by oxidising the growth factor protein and cyclising the peptide by oxidising the growth factor protein and cyclisting the peptide by oxidising the growth factor protein and cyclisting the peptide by oxidising the growth factor protein and cyclisting the peptide with at least one amino acid deleted prior peptides, dimeric bicyclic peptides (comprising 2 linked monocyclic peptides) and a cyclic peptide with at least one amino acid deleted prior corvivation are used to interfere with anglogenesis, conversely to characterised by anglogenesis, neovascularisation or lymphangiogenesis in a mammal with a condition characterised by anglogenesis, neovascularisation or lymphangiogenesis.

The condition is diabetic retinopathy, psoriasis, arthropathy, correbrovascular accident, post-angioplasty restenosis, head, heat or cold crauma, substance-induced neovascularisation of the liver, excessive hormone-related anglogenic dysfunction, diabetes induced neovascular sequelae, hypertension induced neovascular sequelae, are also used to modulate vascular permeability in a mammal (the mammal has a condition characterised by fluid accumulation in peripheral limbs or in lungs, peritoned avity, pleura, or brain. The peptides are used to image blood vessels and lymphatic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Novel monomeric monocyclic peptide, used to interfere with angiogenesis, or lymphangiogenesis, is produced by cyclizing a peptide loop fragment from an exposed loop of a growth factor protein by oxidizing the cysteine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    vasculature. The monomeric and bicyclic peptides are used to interfere with at least one biological activity induced by VEGF, VEGF-C or -D and are also used in combination with an anti-inflammatory agent, to treat a chronic inflammation, especially rheumatoid arthritis, psoriasis and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The sequence represents a monomeric monocyclic peptide of the invention,
                                                                                                                                                                                                                                                                                                                                                               Cendron A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Example 25; Page 47; 102pp; English.
                                                                                                                                                                                                                                                                                                                                                               Stacker S,
                                                                                                                                                                                                                                                                                         (LUDW-) LUDWIG INST CANCER RES
                                                                                                    18-JAN-2001; 2001WO-US001533.
                                                                                                                                                                         18-JAN-2000; 2000US-0176293P.
16-MAY-2000; 2000US-0204590P.
                                                                                                                                                                                                                                                                                                                                                                   Hughes RA,
                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2001-442248/47.
                                                                                                                                                                                                                                                                                                                                                                   Achen MG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          residues.
The sequence represents a monomeric monocyclic peptide of the invention, whose 3-dimensional structure is modelled on the expose loop of human veges (asscular endothelial growth factor). The invention relates to a method of producing a monomeric monocyclic peptide by a measuring beta-ce beta carbon separation distances on opposite antiparallel strands of a peptide loop fragment from an exposed loop of a growth factor protein and cyclising the peptide by oxidising the cysteine residues. The monocyclic peptides, dimeric bicyclic peptides (comprising 2 linked monocyclic peptides) and a cyclic peptide with at least one amino acid deleted prior to cyclistation are used to interfere with angiogenesis,

The condition is diabetic retinopathy, psoriasts, arthropathy, cerebrovascular accident, post-actions the period malignant or benign tumour, post-recovery cerebrovascular accident, post-acidation of the liver, excessive conduction is diabetic retinopathy, psoriasts, activopathy, cerebrovascular accident, post-acidation of the liver, excessive conduction. The peptides are also used to modulate vascular permeability in a committion in peripheral limbs or in lungs, peritoned neovascular sequelae, hypertension induced neovascular sequelae, accumulation in peripheral limbs or in lungs, peritoned acvity, pleura, or brain. The peptides are used to image blood vessels and lymphatic contamilation. The peptides are used to image blood vessels and lymphatic contamilation in peripheral limbs or in lungs, peritoned acvity, pleure or brain. The peptides are used to image blood vessels and lymphatic contamilation with at least one biological activity induced by VBGF. Core D and corporation inflammation, especially rheumatoid arthritis, psoriasis and diabetic retinated and compination with an anti-inflammatory agent, to treat a corporation related and incombination with an intringent activity induced by VBGF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ..
H
                                                                                                                                                                             Novel monomeric monocyclic peptide, used to interfere with angiogenesis, or lymphangiogenesis, is produced by cyclizing a peptide loop fragment from an exposed loop of a growth factor protein by oxidizing the cysteine
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Gaps .. Human; VEGF; vascular endothelial growth factor; angiogenesis; neovascularisation, lymphangiogenesis, psoriasis, tumour; diabetes induced neovascular sequelae, rheumatoid arthritis; Length 11; Indels ; 0 4 OB 74.1%; Score 41.5; DB 72.7%; Pred. No. 2.5; ive 2; Mismatches AAU04544 standard; peptide; 11 AA. VEGF based monocyclic peptide 22. 5, (first entry) Conservative 1 CISVPL-SVPC 10 11 1 CVSVPLTTVPC Local Similarity nes 8; Conserv 26-SEP-2001 AAU04544; Query Match Matches RESULT 7 AAU04544 ò g

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21-NOV-2001 (first entry)
                                                                                                                                             cancer; gene therapy
                                                                                                                                                                                     Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        17-MAR-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .4-AUG-2000;
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                                                                                                                                                                                                                                                                    02-AUG-2001
  AAM95534;
  The sequence represents a monomeric monocyclic peptide of the invention, whose 3-dimensional structure is modelled on the expose loop of human vergeb (vascular endchelal growth factor). The invention relates to a method of producing a monomeric monocyclic peptide by a measuring betace the carbon separation distances on opposite antiparallel strands of a peptide loop fragment from an exposed loop of a growth factor protein and cyclising the peptide by oxidising the cystein residues. The monocyclic peptides, dimeric bicyclic peptides (comprising 2 linked monocyclic peptides) and a cyclic peptide with at least one amino acid deleted prior to cyclisation are used to interfere with angiogenesis.

Cro cyclisation are used to interfere with angiogenesis.

Cro cyclisation or lymphangiogenesis in a mammal with a condition characterised by angiogenesis, neovascularisation or lymphangiogenesis.

Cro cyclisation is diabeted retrinopathy, psoriasis, arthropathy, cerebrovascular accident, post-arinopathy, psoriasis, arthropathy, cerebrovascular accident, post-angioplasty reseenosis, head, heat or cold trauma, substance-induced neovascular sequelae, hypertension induced neovascular sequelae, hypertension induced neovascular sequelae, hypertension indeed novascular sequelae, or chronic liver infection. The peptides are also used to modulate vascular permeability in a mammal (the mammal has a condition characterised by fluid accumulation in peripheral limbs or in lungs, peritoneal cavity, pleura, or brain. The peptides are used to image blood vessels and lymphatic vasculature. The monomeric and bicyclic peptides are also used in combination with an anti-inflammatory agent, to treat a continion inflammation, especially rheumatoid arthritis, psoriasis and diabetic control of the 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      i,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Novel monomeric monocyclic peptide, used to interfere with angiogenesis, or lymphangiogenesis, is produced by cyclizing a peptide loop fragment from an exposed loop of a growth factor protein by oxidizing the cysteine
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                                                                                                                 /note= "This bond cyclises the peptide"
diabetic retinopathy; chronic inflammation; cyclic.
                                                                                                                                                                                                                                                                                                                                                                                          Cendron A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Example 25; Page 47; 102pp; English.
                                                                               Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                          Achen MG, Hughes RA, Stacker S,
                                                                                                                                                                                                                                                                                                                                                 (LUDW-) LUDWIG INST CANCER RES
                                                                                                                                                                                                                                           18-JAN-2001; 2001WO-US001533
                                                                                                                                                                                                                                                                                   18-JAN-2000; 2000US-0176293P
16-MAY-2000; 2000US-0204590P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 CISVPL-SVPC 10
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                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2001-442248/47
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Best Local Similarity
                                                                                                Disulfide-bond
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 11 AA;
                                                                                                                                                              WO200152875-A1
                                                                                                                                                                                                    26-JUL-2001
                                      Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     residues.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Novel
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AAM95534
ID AAM9
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AAM95534 standard; protein; 77 AA.

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Human; reproductive system related antigen; reproductive system disorder;
Human reproductive system related antigen SEQ ID NO: 4192.
                                                                                                                                                                                                                                                                          2000US-0189874P.
2000US-0190076P.
2000US-0198123P.
2000US-0205515P.
2000US-0209467P.
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2000US-0217496P.
2000US-0219629P.
2000US-0220963P.
2000US-0220964P.
2000US-0224519P.
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2000US-0225270P.
2000US-022547P.
2000US-022577P.
2000US-0225758P.
2000US-0225758P.
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2000US-0225214P.
2000US-0225266P.
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2000US-0229345P.
2000US-0229509P.
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2000US-0230438P.
2000US-0231242P.
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2000US-0186350P.
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2000US-0227182P.
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Isolated nucleic acid molecule encoding a reproductive system antigen is used in preventing, treating or ameliorating a medical condition.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human; testicular antigen; testes; cancer; metastasis; immune disorder; reproductive system disorder; urinary system disorder; gene therapy; cardiovascular disorder; respiratory disorder; neurological disorder; gastrointestinal disease; infection; cytostatic.
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                                                                                                                                                                                                                                              Claim 11; SEQ ID NO 4192; 1297pp + Sequence Listing; English.
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40.0%; Pred. No. 48;
ive 4; Mismatches 2; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ABB96216 standard; protein; 77 AA
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08-DEC-2000; 2000US-0251856P.

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                                                                                                         (HUMA-) HUMAN GENOME SCI INC
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Best Local Similarity 40.0
Matches 4; Conservative
                                                                                                                                      Rosen CA, Barash SC,
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CLNAPIRIPC 56
                                                                                                                                                               WPI; 2001-465570/50.
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06-DEC-2000; 2
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Rosen CA, Barash SC,

WPI; 2001-483232/52

Nucleic acids encoding 973 human testicular antigen polypeptides, useful for preventing, diagnosing and/or treating testicular cancer.

Claim 11; SEQ ID NO 1600; 766pp; English

of 973 The present invention provides the protein and coding sequences of 973 human testicular antigens, and fragments of their genomic sequences. The sequences can be used in the treatment of cardiovascular, urinary system reproductive system, immune, respiratory, neurological and gastrointestinal disorders, infections, and particularly cancer, especially testicular cancers. The present sequence is a protein of the invention

Sequence 77 AA;

Score 39; DB 4; Length 77; Pred. No. 48; 69.6%; Query Match Best Local Similarity

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Pred. No. 68;
1; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ABB96358 standard; protein; 108 AA.
                                                                                                                                                                                                                                               Ruben SM;
17-NOV-2000; 2000US-0249264P.
17-NOV-2000; 2000US-0249265P.
17-NOV-2000; 2000US-0249299P.
17-NOV-2000; 2000US-0249299P.
17-NOV-2000; 2000US-0249390P.
17-NOV-2000; 2000US-0249300P.
01-DEC-2000; 2000US-025919P.
05-DEC-2000; 2000US-025198P.
06-DEC-2000; 2000US-025198P.
06-DEC-2000; 2000US-0251866P.
08-DEC-2000; 2000US-0251868P.
08-DEC-2000; 2000US-0251869P.
08-DEC-2000; 2000US-0251869P.
08-DEC-2000; 2000US-0251989P.
08-DEC-2000; 2000US-0251989P.
08-DEC-2000; 2000US-0251989P.
08-DEC-2000; 2000US-0251989P.
08-DEC-2000; 2000US-0251989P.
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04-FEB-2000; 2000US-0180628P.
24-FEB-2000; 2000US-0184664P.
                                                                                                                                                                                                                        (HUMA-) HUMAN GENOME SCI INC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity 77.8
                                                                                                                                                                                                                                                                                                                                                                                                                                            69.
                                                                                                                                                                                                                                              Barash SC,
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                                                                                                                                                                                                                                                                   WPI; 2001-465570/50.
N-PSDB; AAL01797.
                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 108 AA
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                                                                                                                                                                                                                                              Rosen CA,
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Best Local S
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sequences can be used in the treatment of cardiovascular, urinary system, reproductive system, immune, respiratory, neurological and gastrointestinal disorders, infections, and particularly cancer, especially testicular cancers. The present sequence is a protein of the human testicular antigens, and fragments of their genomic sequences. The

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Gaps

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Length 108; Indels

69.6%; Score 39; DB 4; 77.8%; Pred. No. 68; ive 1; Mismatches

Conservative

Query Match Best Local Similarity Matches 7; Conserv

Sequence 108 AA;

88888888888

2 ISVPLSVPC 10

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Nucleic acids encoding 973 human testicular antigen polypeptides, useful for preventing, diagnosing and/or treating testicular cancer.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 11; SEQ ID NO 1742; 766pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Rosen CA, Barash SC, Ruben SM
                                                                                                               2000US-0246475P.
2000US-0246476P.
2000US-0246477P.
                                                                                                                                        2000US-0246478P.
2000US-0246523P.
2000US-0246524P.
                                                                                                                                                                   2000US-0246525P.
2000US-0246526P.
2000US-0246527P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (HUMA-) HUMAN GENOME SCI INC.
                                         2000US-0241785P.
2000US-0241786P.
2000US-0241787P.
                        2000US-0240960P
                                                                                     2000US-0241826P.
2000US-0244617P.
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2000US-0249214P.
                                                                     2000US-0241808P
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                      20-0CT-2000;
20-0CT-2000;
20-0CT-2000;
20-0CT-2000;
20-0CT-2000;
20-0CT-2000;
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05-DEC-2000;
06-DEC-2000;
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08-NOV-2000;
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08-NOV-2000;
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08-NOV-2000;
08-NOV-2000;
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08-NOV-2000;
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08-NOV-2000;
                                                                                     20-OCT-2000;
01-NOV-2000;
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17-NOV-2000;
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05-DEC-2000;
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The sequence represents a monomeric monocyclic peptide of the invention, whose 3-dimensional structure is modelled on the expose loop of human VEGPD (vascular endothellal growth factor). The invention relates to a method of producing a monomeric monocyclic peptide by a measuring betabeta carbon separation distances on opposite antiparallel strands of a peptide loop fragment from an exposed loop of a growth factor protein and cyclising the peptide by oxidising comprising 2 linked monocyclic peptides, dimeric bicyclic peptides (comprising 2 linked monocyclic peptides) and a cyclic peptide with at least one amino acid deleted prior to cyclisation are used to interfere with angiogenesis, neovascularisation or lymphandiogenesis in a mammal with a condition characterised by angiogenesis, neovascularisation or lymphangiogenesis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Novel monomeric monocyclic peptide, used to interfere with angiogenesis, or lymphangiogenesis, is produced by cyclizing a peptide loop fragment from an exposed loop of a growth factor protein by oxidizing the cysteine
                                                                                                                                                                                                                                               Human; VEGF; vascular endothelial growth factor; angiogenesis;
                                                                                                                                                                                                                                                                neovascularisation, lymphangiogenesis; psoriasis; tumour; diabetes induced neovascular sequelae; rheumatoid arthritis; diabetic retinopathy; chronic inflammation; cyclic.
                                                                                                                                                                                                                                                                                                                                                                                                           /note= "This bond cyclises the peptide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Cendron A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Example 25; Page 47; 102pp; English.
                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Stacker S,
                                                                                                   AAU04543 standard; peptide; 11 AA
                                                                                                                                                                                                             VEGF based monocyclic peptide 21.
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16-MAY-2000; 2000US-0204590P.
                                                                                                                                                                         entry)
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         41
                                                                                                                                                                         (first
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33 VSVPLSHPC
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Disulfide-bond
                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO200152875-A1.
                                                                                                                                                                       26-SEP-2001
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                                                                                                                                                                                                                                                                                                                                        Synthetic
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                                                                                                                                     AAU04543;
                                                                 RESULT 12
                                                                                    AAU04543
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The condition is diabetic retinopathy, psoriasis, arthropathy, he menagions, vascularised malignant or benign tumour, post-recovery cerebrovascular accident, post-angioplasty restenosis, head, heat or cold trauma, substance-induced neovascularisation of the liver, excessive bormone-related angiogenic dysfunction, diabetes induced neovascular sequelae, or chronic liver sequelae, hypertension induced neovascular sequelae, or chronic liver infection. The peptides are also used to modulate vascular permeability in a mammal (the mammal has a condition characterised by fluid communitation in peripheral limbs or in lungs, peritoneal cavity, pleura, or brain. The peptides are used to image blood vessels and lymphatic vasculature. The monomeric and bicyclic peptides are used to interfere with at least one biological activity induced by VEGF, VEGF-C or -D and are also used in combination with an anti-inflammatory agent, to treat a chronic inflammation, especially rheumatoid arthritis, psoriasis and diabetic retinopathy
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                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder.
                                                                                                                                                                                                                                                                                                                                                                                                 1;
                                                                                                                                                                                                                                                                                                                                                      68.8%; Score 38.5; DB 4; Length 11; 63.6%; Pred. No. 7.8; ive 3; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 20; SEQ ID NO 42901; 103pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Novel human diagnostic protein #12533
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ABG12542 standard; protein; 59 AA.
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2000US-00649167
                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 63.0.,
7; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                  1 CISVPL-SVPC 10
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CITIPLTSLPC 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         N-PSDB; AAS76729
                                                                                                                                                                                                                                                                                                                  Sequence 11 AA;
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           Purpyperior in the binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polymcleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations are seponsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and amino acid sequences. ABG00010-ABG30377 represent novel human diagnostic patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO at Eftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to isolated polymucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain raction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polymucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging
                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
 polypeptide in tissue, as molecular weight markers and as a food
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder.
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                                                                                                                                                                                                                                                                                                   4; Length 59;
                                                                                                                                                                                                                                                                                                                                        2; Indels
                                                                                                                                                                                                                                                                                               67.9%; Score 38; DB 70.0%; Pred. No. 53; ive 1; Mismatches
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23-AUG-2000; 2000US-00649167.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                    Best_Local Similarity 70.0
Matches 7; Conservative
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N-PSDB; AAS76717.
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                                                                                                                                                                                                                                                                Sequence 59 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human genome-derived single exon nucleic acid probes useful for analyzing gene expression in human cervical epithelial cells.
of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and amino acid sequences. ABG00010-ABG30377 represent novel human diagnostic patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO at the invito.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Peptide #2437 encoded by probe for measuring cervical gene expression.
                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Probe; human; microarray; gene expression; cervical epithelial cell;
                                                                                                                                                                                                                                                                     .
                                                                                                                                                                                                                                   4; Length 59;
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53;
                                                                                                                                                                                                                                                                     1; Mismatches
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                                                                                                                                                                                                                                   Score 38;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Chen W, Rank DR;
                                                                                                                                                                                                                                                                                                                                                                                                                  AAM16003 standard; protein; 71 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (MOLE-) MOLECULAR DYNAMICS INC
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2000US-0234687P.
2000US-0236359P.
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2000US-00608408.
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                                                                                                                                                                                                                                                                     7; Conservative
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9 CISVLVPVPC 18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2001-488901/53
                                                                                                                                                                                                                                   Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     cervical cancer.
                                                                                                                                                                                                    Sequence 59 AA;
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21-SEP-2000;
27-SEP-2000;
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                         Score 38; DB 4; Length 71; Pred. No. 65;
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                                            Mismatches
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                         67.98;
                Query Match
Best Local Similarity 7/...
7/...
7/. Conservative
                                                                                                               Search completed: September
Job time: 34,8283 secs
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                                                              1 CISVPLSVP
       Sequence 71 AA;
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; Sequence 7, Application US/09761636A
; Patent No. US20020065218A1
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US-09-761-636A-7
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Sequence 58210, A
Sequence 4485, Ap
Sequence 50298, A
Sequence 24, Appl
Sequence 35705, A
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Sequence 23, Appli
Sequence 174203,
Sequence 14, Appl
Sequence 26, Appl
Sequence 26, Appl
Sequence 26, Appl
Sequence 25, Appl
Sequence 157987,
                                                                                                                                 5 ; Search time 28.0808 Seconds (without alignments) 112.199 Million cell updates/sec
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| cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep:*
| cgn2_6/ptodata/2/pubpaa/PCT_MBW_PUB_pep:*
| cgn2_6/ptodata/2/pubpaa/PCT_MBW_PUB_pep:*
| cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB_pep:*
| cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB_pep:*
| cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB_pep:*
| cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB_pep:*
| cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB_pep:*
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| cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB_pep:*
| cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB_pep:*
| cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB_pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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16 US-09-761-636A-24

9 US-09-761-636A-14

12 US-09-761-636A-26

12 US-09-761-636A-26

12 US-09-761-636A-26

13 US-09-761-636A-26

14 US-10-45-59-264847

15 US-10-43-963-167-987

16 US-10-425-114-58210

10 US-09-764-891-4485

10 US-09-764-891-4485

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Maximum Match 100%
Listing first 45 summaries
                                                                                       OM protein - protein search, using sw model
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Maximum DB seq length: 200000000
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1 CISVPLSVPC 10
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Match Length DB
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                                                                                                                                                                                                                      Title:
Perfect score:
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Sequence 140110,
Sequence 2238, Ap
Sequence 7910, Ap
Sequence 7911, Ap
Sequence 7911, Ap
Sequence 7912, Ap
                                                                                                                    Sequence 754, App
Sequence 29825, A
Sequence 268, App
Sequence 10647,
Sequence 106647,
Sequence 2, Appli
Sequence 2, Appli
Sequence 3554, Ap
Sequence 7, Appli
Sequence 7, Appli
Sequence 7, Appli
Sequence 7, Appli
Sequence 119123,
Sequence 576, App
Sequence 576, Appli
                                                                                    Sequence 6, Appli
Sequence 2, Appli
Sequence 284943,
Sequence 199587,
                                                           Sequence 4531, Ap
Sequence 125857,
Sequence 142446,
2 US-10-424-599-220123

6 US-10-437-963-140110

2 US-10-346-047-238

2 US-10-346-047-238

2 US-10-335-977-7911

2 US-10-335-977-7911

2 US-10-335-977-7911

2 US-10-335-977-7911

2 US-10-437-963-142446

3 US-10-437-963-142446

3 US-10-687-110-2

4 US-10-087-110-2

5 US-10-427-963-199587

4 US-10-087-186-8

6 US-10-427-963-199587

4 US-10-087-186-8

6 US-10-424-599-198582

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8 US-09-915-576
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578
616
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134
355
420
769
875
 35.5
35.5
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ALIGNMENTS

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SQUENCE 13, Application US/09761636A

SQUENCE 13, Application US/09761636A

SQUENCE 13, Application US/09761636A

GENERAL INFORMATION:

APPLICANT: ACHEN, Mach
APPLICANT: GTACKER, Steven
APPLICANT: HUGHES, Richard
APPLICANT: HUGHES, Richard
APPLICANT: HUGHES, Richard
APPLICANT: HUGHES, Richard
CURRENT FILEOF INVENTION: VEGF-C/VEGF PEPTIDOMIMETIC INHIBITOR
FILE REFERENCE: 1064/48505 Achen et al
CURRENT PILLON NUMBER: US/09/761,636A
CURRENT PILLON DATE: 2000-10-18
PRIOR PILLON DATE: 2000-01-18
PRIOR PLILON DATE: 2000-01-18
PRIOR PLILON DATE: 2000-01-16
NUMBER OF SEQ ID NOS: 34

SOFTWARE: PatentIn version 3.0

SEQ ID NO 13

LENGTH: 10
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ORGANISM: Homo sapiens
US-09-761-636A-13
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Best Local Similarity
Matches 10; Conserv
RESULT 1
US-09-761-636A-13
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Gaps

CISVPLSVPC 10 1 CISVPLSVPC 10

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APPLICANT: Barbazuk, Brad
APPLICANT: Barbazuk, Brad
TITLE OF INVENTION: Plants and Wes Thereof for Plant Improvement
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
CURRENT APPLICATION WINBER: US/10/437,963
CURRENT FILING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
SEQ ID NO 174203
LENTH: 140
TYPE: PP"
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Patent No. US20020065218A1

GENERAL INFORMATION:

APPLICANT: APPLICANT: STACKER, Steven

APPLICANT: STACKER, Steven

APPLICANT: CENDROW, Angle

TITLE OF INVENTION: VEGF-C/VEGF PEPTIDOMIMETIC INHIBITOR

FILE REFERENCE: 1064/48505 Achen et al

CURRENT APLICATION NUMBER: US/09/761,636A

CURRENT FILING DATE: 2000-01-18

PRIOR APPLICATION NUMBER: US 60/176,293

PRIOR FILING DATE: 2000-01-18

PRIOR FILING DATE: 2000-05-16

NUMBER OF SEQ ID NOS: 34

SEQ ID NOS: 34

SEQ ID NOS: 34

SEQ ID NO 14

FENDRE PERCENTIAL PATENTIAL PATENT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; OTHER INFORMATION: Clone ID: PAT_MRT4530_72167C.1.pep
US-10-437-963-174203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LOCATION: (1)..(140)
OTHER INFORMATION: unsure at all Xaa locations
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; APPLICANT: ACHEN, Marc
APPLICANT: STACKER, Steven; APPLICANT: HUGHES, Richard
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity 90.0
Matches 9, Conservative
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Best Local Similarity 70.0
Matches 7; Conservative
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
ORGANISM: Oryza sativa
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US-09-761-636A-26
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; Sequence 23, Application US/09761636A
; Patent No. US20020065218A1
; GENERAL INFORMATION:
    APPLICANT: ACHEN, Marc
    APPLICANT: CENDROW, Angela
    APPLICANT: HUGHES, Richard
    APPLICANT: HUGHES, Richard
    APPLICANT: HUGHES, Richard
    TILLE OF INVENTION: USGF-C/VEGF PEPTIDOMIMETIC INHIBITOR
    TILLE OF INVENTION: USGF-C/VEGF PEPTIDOMIMETIC INHIBITOR
    TURENT APPLICATION NUMBER: US/09/761,636A
    CURRENT APPLICATION NUMBER: US 60/176,293
    PRIOR PLILING DATE: 2000-01-18
    PRIOR PLILING DATE: 2000-01-18
    PRIOR PLILING DATE: 2000-05-16
    NUMBER OF SEQ ID NOS: 34
    SOFTWARE: Patent In version 3.0
; SEQ ID NO 23
    LENGTH: 1
                                                                                                                                                                     APPLICANT: ACHEN, Marc
APPLICANT: STACKER, Steven
APPLICANT: STACKER, Steven
APPLICANT: STACKER, Steven
APPLICANT: STACKER, Steven
APPLICANT: CENDRON, Angela
TITLE OF INVENTION: VEGF-D/VEGF-C/VEGF PEPTIDOMIMETIC INHIBITOR
FILE REFERENCE: 1064/48505 Achen et al
CURRENT APPLICATION NUMBER: US 60/176,293
PRIOR APPLICATION NUMBER: US 60/176,293
PRIOR PILING DATE: 2000-01-18
PRIOR PLLING DATE: 2000-01-16
PRIOR FILING DATE: 2000-01-16
PRIOR FILING DATE: 2000-05-16
NUMBER OF SEQ ID NOS: 34
SOFTWARE: Patentin version 3.0
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Pred. No. 2.3;
1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 45.5; DB 9; Length 11;
Pred. No. 1.1;
0; Mismatches 0; Indels
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PUblication No. US20040123343A1
GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Caou, Yihua
APPLICANT: Cao, Yongwei
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 81.2%;
Best Local Similarity 90.9%;
Matches 10; Conservative (
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US-09-761-636A-23
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Best Local Similarity 81.8%;
Matches 9; Conservative
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1 CLSVPLTSVPC 11
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ORGANISM: Homo sapiens
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US-09-761-636A-23
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Sequence 167987, Application US/10437963
; Sequence 167987, Application No. US20040123343A1
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Zhou, Yihua
; APPLICANT: Zhou, Yihua
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Brandard, Brad
; APPLICANT: Brandard, Brad
; APPLICANT: Brandard, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; TITLE OF INVENTION: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; WUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 167987
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; Publication No. US20030077808A1
; GENERAL INFORMATION:
    APPLICANT: Rosen et al.
    TITLE OF INVENTION: Mucleic Acids, Proteins, and Antibodies
    TITLE REFERENCE: PC006
; CURRENT APPLICATION NUMBER: US/09/764,891
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - consult PALM or file wrapper
; SOFTWARE: Patentin Ver: 2.0
; SEQ ID NO 4192
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; OTHER INFORMATION: Clone ID: PAT_MRT4530_66546C.1.pep US-10-437-963-167987
                                                                                                                                                                                                                                                                         0;
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Pred. No. 6.7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                71.4%; Score 40; DB 16; 77.8%; Pred. No. 1.8e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: unsure
LOCATION: (1)..(279)
OTHER INFORMATION: unsure at all Xaa locations
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1; Mismatches
  PRIOR APPLICATION NUMBER: US 60/204,590
PRIOR FILING DATE: 2000-05-16
NUMBER OF SEQ ID NOS: 34
SOFTWARE: PatentIn version 3.0
SEQ ID NO 25
LENGTH: 11
                                                                                                                                                                                                                            72.3%;
                                                                                                                                         ; TYPE: PRT
; ORGANISM: synthetic construct
US-09-761-636A-25
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Best Local Similarity 77.8
Matches 7; Conservative
                                                                                                                                                                                                                                               Best Local Similarity 72.7
Matches 8, Conservative
                                                                                                                                                                                                                                                                                                                     1 CISVPL-SVPC 10
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ORGANISM: Oryza sativa
FEATURE:
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US-09-764-891-4192
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US-10-424-599-264847
US-10-424-599-264847
Sequence 264847
Publication No. US20040031072A1
Sequence 26487, Application US/10424599
Publication No. US20040031072A1
Sequence 26487, Application No. US20040031072A1
APPLICANT: La Rosa Thomas J
APPLICANT: Zhou Yihua
APPLICANT: Zhou Yihua
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REPERBENCE: 38-21(53223)8
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
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; Patent No. US2002065218A1
; GENERAL INFORMATION:
; APPLICANT: ACHEN, Marc
; APPLICANT: STACKER, Steven
; APPLICANT: HUGHES, Richard
; APPLICANT: CENDRON, Angela
; TITLE OP INVENTION: VEGF-D/VEGF-C/VEGF PEPTIDOMIMETIC INHIBITOR
; FILE REFERENCE: 1064/48505 Achen et al
; CURRENT APPLICATION NUMBER: US/09/761,636A
; CURRENT FILING DATE: 2001-01-18
; PRIOR FILING DATE: 2000-01-18
HAPLICANT: CENDRON, Angela
TITLE OF INVENTION: VEGF-D/VEGF-C/VEGF PRPTIDOMIMETIC INHIBITOR
FILE REPERENCE: 1064/48505 Achen et al
CURRENT APPLICATION NUMBER: US/09/761,636A
CURRENT PILING DATE: 2001-01-18
PRIOR APPLICATION NUMBER: US 60/176,293
PRIOR PILING DATE: 2000-01-18
PRIOR PILING DATE: 2000-01-18
PRIOR FILING DATE: 2000-05-16
NUMBER OF SEQ ID NOS: 34
SEQ ID NO 26
LENGTH: 11
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Pred. No. 39;
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US-10-424-599-264847
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Pred. No. 4.7;
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                                                                                                                                                                                                                                                                                                                   ; ORGANISM: synthetic construct
US-09-761-636A-26
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Best Local Similarity 72.7
Best Local Similarity 72.7
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Best Local Similarity 70.0
Matches 7; Conservative
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1; Mismatches
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                                                                                                                                                                                                                                                                                         69.6%;
                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 77.8
Section 7; Conservative
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Best Local Similarity 75.0
Matches 6; Conservative
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ORGANISM: Zea mays
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                                              NAME/KEY: SITE
                                                                                                                                                                              NAME/KEY: SITE
                                                                                                                                      (73)
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                                                                                                                                      LOCATION:
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APPLICANT: Liu, Jingdong
APPLICANT: Zhou, Yihua
APPLICANT: Shoul Seven E
APPLICANT: Screen, Seeven E
APPLICANT: Screen, Jack E
APPLICANT: Tabaska, Jack E
APPLICANT: Tabaska, Jack E
APPLICANT: Tabaska, Jack E
APPLICANT: Tabaska, Jack E
APPLICANT: Screen, Solvential Seeven E
APPLICANT: Tabaska, Jack E
APPLICANT: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
CURRENT APPLICATION NUMBER: US/10/425,114
CURRENT FILING DATE: 2003-04-28
SEQ ID NOS: 73128
LENGTH: 83
LENGTH: 83
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                                  FEATURE:

NAME/KEY: SITE

LOCATION: (38)

OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids

LOCATION: (65)

COTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids

COTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids

US-09-764-891-4192
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CURRENT FILING DATE: 2001-01-17
Prior application data removed - consult PALM or file wrapper NUMBER OF SEQ ID NOS: 10231
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 4485
LENGTH: 108
                                                                                                                                                                                                                                           Query Match 69.6%; Score 39; DB 10; Length 77; Best Local Similarity 40.0%; Pred. No. 74; Matches 4; Conservative 4; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          69.6%; Score 39; DB 12; Length 83; 75.0%; Pred. No. 80; tive 2; Mismatches 0; Indels
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Publication No. US20030077808A1
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PC006
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; OTHER INFORMATION: Clone ID: LIB84-029-E3_FLI.pep
US-10-425-114-58210
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Publication No. US20040034888A1
GENERAL INFORMATION:
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Best Local Similarity 75. v.
                                                                                                                                                                                                                                                                                                                                 1 CISVPLSVPC 10
                                                                                                                                                                                                                                                                                                                                                               47 CLNAPIRIPC 56
TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT
ORGANISM: Homo sapiens
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68 TVPLSIPC 75
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US-09-764-891-4485
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Sequence 50298 Application US/10425114

Publication No. US20040034888A1

GENERAL INCORMATION:
APPLICANT: Liu, Jingdong
APPLICANT: Zhou, Yihua
APPLICANT: Zorean, Steven E
APPLICANT: Application Nacleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53313)8
CURRENT APPLICATION NUMBER: US/10/425,114
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 73128
SEQ ID NOS: 73128
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                                                                                                                                                                                                                                                            ; LOCATION: (93)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids US-09-764-891-4485
                                                            LOCATION: (51)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
NAME/KEY: SITE
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
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APPLICANT: STACKER, Steven
APPLICANT: HUGHES, Richard
APPLICANT: CRNDRON, Angela
TITLE OF INVENTION: VEGF-C/VEGF PEPTIDOMIMETIC INHIBITOR
TITLE OF INVENTION: VEGF-D/VEGF-C/VEGF PEPTIDOMIMETIC INHIBITOR
TITLE REFERENCE: 1064/48505 Achen et al
CURRENT APPLICATION NUMBER: US/09/761,636A
CURRENT PILING DATE: 2001-01-18
PRIOR PILING DATE: 2000-01-18
PRIOR APPLICATION NUMBER: US 60/176,293
PRIOR APPLICATION NUMBER: US 60/204,590
                                                                                                                                                                                                                                                                                                                                                                                    Score 39; DB 10; Length 108; Pred. No. 1e+02;
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Gaps

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FEATURE:
CTHER INFORMATION: MAP TO AL078621.19
CTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 0.91
CTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 0.94
CTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 2.7
CTHER INFORMATION: EST HUMAN HIT: BF125501.1, EVALUE 1.70e+00
GTHER INFORMATION: SWISSPROT HIT: P11992, EVALUE 2.20e-01
US-09-864-761-35705
                                                                                                                                                                                                                                                                                                                         Score 38; DB 9; Length 71;
Pred. No. 98;
0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5, 2004, 10:29:23
                                                                                                                                                                                                                                                                                                                         Query Match 67.9%;
Best Local Similarity 77.8%;
Matches 7; Conservative
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Job time: 29.0808 secs
          ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 CISVPLSVP 9
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APPLICANIT. HAIR, DAVIG K.
APPLICANIT. HAIR, DAVIG K.
APPLICANIT. HAIR, DAVIG K.
APPLICANIT. CHEM, MARIBERING
APPLICANIT. CHEM, MARIBERING
FILE REPRENCE: Accord.ca.X.I.
FILE DE INVERTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
FILE MEDICATION WINDER: US/06/864,761
CURRENT PALLING DATE: 2000-02-33
RELOR FILING DATE: 2000-02-33
RELOR FILING DATE: 2000-02-33
RELOR FILING DATE: 2000-02-33
RELOR FILING DATE: 2000-02-34
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RELOR FILIN
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Best Local Similarity 63.6%; Pred. No. 14;
Matches 7; Conservative 3; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 35705, Application US/09864761
Patent No. US20020048763A1
GENERAL INFORMATION:
PRIOR FILING DATE: 2000-05-16
NUMBER OF SEQ.ID NOS: 34
SOFTWARE: PatentIn version 3.0
SEQ.ID NO 24
LENGTH: 11
                                                                                                                                                            ; TYPE: PRT
; ORGANISM: synthetic construct
US-09-761-636A-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Penn, Sharron G. APPLICANT: Rank, David R. APPLICANT: Hanzel, David K.
                                                                                                                                                                                                                                                                                                                                                                                                                       1 CISVPL-SVPC 10
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| CITIPLISLPC 11
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Sequence 32454, A Sequence 23169, A Sequence 23382, A Sequence 133, Appl Sequence 143, Appl Sequence 29933, A Sequence 2665, A Sequence 2663, A Sequence 2663, A Sequence 145, Appl Sequence 58, Appl Sequence 58, Appl Sequence 26, Appl Sequence 27, Appl Sequence 27, Appl Sequence 26, Appl Sequence 27, Appl Sequence 27,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                5, 2004, 09:55:30 ; Search time 8.88889 Seconds (without alignments) 58.079 Million cell updates/sec
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Sequence
Sequence
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/cgm2_6/prodata/2/iaa/5B_COMB.pep:*
/cgm2_6/prodata/2/iaa/6A_COMB.pep:*
/cgm2_6/prodata/2/iaa/6B_COMB.pep:*
/cgm2_6/prodata/2/iaa/PcTUS_COMB.pep:*
/cgm2_6/prodata/2/iaa/PcTUS_COMB.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-09-252-991A-21369

US-09-252-991A-18044

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US-08-331-333-33

US-08-34-008-43

US-08-94-143

US-08-252-991A-29934

US-09-252-991A-29934

US-09-252-991A-29944

US-09-252-991A-26663

US-09-252-991A-26663

US-09-252-991A-26663

US-09-252-991A-26663

US-09-252-991A-2663

US-09-334-951-58

US-09-334-951-56

US-08-334-951-57

US-09-334-951-57

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US-09-334-953A-57
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                                                                                                                                                                                                                                                                                                                                                                                                                                        389414 seqs, 51625971 residues
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Maximum Match 100%
Listing first 45 summaries
                                                                                                     - protein search, using sw model
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Minimum DB seq length: 0 Maximum DB seq length: 2000000000
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                                                                                                                                                                                                                                                                                                     1 CISVPLSVPC 10
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Match Length
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                                                                                                                                                                                                                                                        Title:
Perfect score:
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Sequence 39, Appl Sequence 55, Appl Sequence 55, Appl Sequence 57, Appl Sequence 54, Appl Sequence 59, Appl Sequence 59, Appl Sequence 54, Appl Sequence 54, Appl Sequence 56, Appl Sequence 57, Appl Sequence 57, Appl Sequence 58, Appl Sequence 54, Appl Sequence 56, Appl Sequence 56, Appl Sequence 57, Appl Sequence 57, Appl Sequence 58, Appl Sequence 59, Appl	SEQUENCES RELATING TO PSEUDOMONAS	244; els 0; Gaps 0;	SEQUENCES RELATING TO PSEUDOMONAS ND THERAPEUTICS
74 4 US-09-689-693-39 75 3 US-08-722-719-55 75 4 US-09-334-9234-55 75 4 US-09-334-9234-55 76 3 US-08-722-719-24 76 3 US-08-722-719-56 76 4 US-09-334-951-54 76 4 US-09-334-951-56 76 4 US-09-334-951-56 76 4 US-09-334-951-56 76 4 US-09-334-951-56 76 4 US-09-334-951-57 76 4 US-09-334-923A-56 76 4 US-09-334-923A-56 76 4 US-09-334-953A-56 76 4 US-09-334-954A-56 76 4 US-09-334-954A-56 76 4 US-09-334-954A-59 76 4 US-09-334-954A-59	ALIGNMENTS ion US/09252991A confield et al. CLEIC ACID AND AMINO ACII RUGINOSA FOR DIAGNOSTICS 5.136 HBR: US/09/252,991A 999-02-18 R: US 60/074,788 R: US 60/074,190 98-07-27 33142 aeruginosa	69.6%; Score 39; DB 4; Length 60.0%; Pred. No. 44; ative 2; Mismatches 2; Ind 10	MINO ACID GNOSTICS A 91A 8
28 34.5 61.6 31.3 34.5 61.6 31.3 34.5 61.6 32.3 34.5 61.6 33.3 34.5 61.6 34.5 61.6 37.3 34.5 61.6 37.3 34.5 61.6 40.3 34.5 61.6 41.3 34.5 61.6 42.3 34.5 61.6 43.3 34.5 61.6 44.3 34.5 61.6 44.3 34.5 61.6 45.3 61.6 46.4 34.5 61.6	RESULT 1 US-09-252-991A-32454 ; Sequence 32454, Applicat ; Patent No. 6551795 ; GENERAL INCEMATION: TITLE OF INVENTION: TITLE OF INVENTION: TITLE OF INVENTION: CURRENT FILING DATE: 107194 CURRENT FILING DATE: 195 ; PRIOR PELICATION NUMBE; PRIOR FILING DATE: 195 ; NUMBER OF SEQ ID NOS: SEQ ID NO 32454 LENGTH: 244 ; TYPE: PRT	Query Match Best Local Similarity 60. Matches 6; Conservative Oy 1 CISVPLSVPC 10 Db 24 CCSRPMAVPC 33	RESULT 2 US-09-252-991A-23169 Sequence 23169, Application US/09252991A Patent No. 6551795 GENERAL INFORMATION: APPLICANT: MARC J. Rubenfield et al. TITLE OF INVENTION: NUCLEIC ACID AND AL. FILE REFERENCE: 107196.136 CURRENT APPLICATION NUMBER: US/09/252, 9 CURRENT APPLICATION NUMBER: US 60/074,78 PRIOR FILING DATE: 1999-02-18 PRIOR FILING DATE: 1998-02-18 PRIOR FILING DATE: 1998-07-27 NUMBER OF SEQ ID NOS: 33142 LENGTH: 306 LENGTH: 306 TYPE: PRT

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Conservative
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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Best Local Similarity
Matches 4; Conserv
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APPLICANT: MATC J. Rubenfield et al.

TITLE OF INVENITION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS TITLE OF INVENITION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS FILE REFERENCE: 107196.136

CURRENT PAPLICATION NUMBER: US 00/09/252,991A

PRIOR PILING DATE: 1999-02-18

PRIOR FILING DATE: 1999-02-18

PRIOR FILING DATE: US 60/094,190

PRIOR FILING DATE: 1998-07-27

NUMBER OF SEQ ID NOS: 33142
                                                                                                                                                                                                                                                                                                                 APPLICANTION:
APPLICANT: MATC J. Rubenfield et al.
APPLICANT: MATC J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS FILE REFERENCE: 107196.136
CURRENT PAPLICATION NUMBER: US/09/252,991A
CURRENT PILING DATE: 1999-02-18
PRIOR FILING DATE: 1999-02-18
PRIOR FILING DATE: US/00/074,788
PRIOR FILING DATE: US/00/074,788
PRIOR FILING DATE: US/00/074,789
PRIOR FILING DATE: US/00/074,789
NRIOR FILING DATE: US/00/074,789
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 37; DB 4; Length 142;
Pred. No. 52;
2; Mismatches 3; Indels
                                                           Length 306;
                                                                                                   Indels
                                                        Query Match 69.6%; Score 39; DB 4; Best Local Similarity 70.0%; Pred. No. 55; Matches 7; Conservative 0; Mismatches 3
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; Sequence 23382, Application US/09252991A
; Patent No. 6551795
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; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-23169
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50.0%;
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50.0%;
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Best Local Similarity 50.v
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137 CSSLPMRLPC 146
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89 CLPPPISAPC 98
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Best Local Similarity
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LENGTH: 154
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LENGTH: 142
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Sequence 29933, Application US/09252991A

Faceur No. 6551795

GENERAL INFORMATION:

APPLICATION:

MILE REPERROR:

TITLE OF INVENTION:

ARRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

TITLE OF INVENTION:

TITLE OF INVENTION:

ARRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

TITLE OF INVENTION:

FILE REPERROR:

FILE REPERROR:

PRIOR FILING DATE: 1999-02-18

PRIOR PAPLICATION NUMBER: US 60/074,788

PRIOR PLING DATE: 1998-02-18

PRIOR FILING DATE: 1998-02-18

PRIOR FILING DATE: 1998-02-18

PRIOR FILING DATE: 1998-02-18

PRIOR FILING DATE: 1998-07-17

NUMBER OF SEQ ID NOS: 33142

LENGTH: 92
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                                                                                                                         Length 9;
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APPLICANT: Jobert, S.
TITLE OF INVENTION: ESTS and Encoded Human Proteins.
FILE REFERENCE: GENET.054PR2
CURRENT APPLICATION NUMBER: US/09/621,976
CURRENT FILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 19335
SOFTWARE: Patent.pm
SEQ ID NO 5605
LENGTH: 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 36; DB 4;
Pred. No. 48;
3; Mismatches
                                                                                                                    Score 36; DB 3;
Pred. No. 3e+05;
4; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
APPLICANT: Dumas Milne Edwards, J.B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Pseudomonas aeruginosa US-09-252-991A-29933
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     64.3%;
                                                                                                                         64.3%;
50.0%;
                                                                                                                                                                Conservative
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Best Local Similarity 55.6
Matches 5; Conservative
                                                           ; MOLECULE TYPE: peptide US-08-802-981-143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 CISVPLSVPC 10
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ORGANISM: Homo sapiens
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 ISVPLSVPC 10
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33 VEVPVAVPC 41
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2 AIPMSIPC 9
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Best Local Similarity
Matches 5; Conserv
                                                                                                                      Query Match
Best Local Similarity
Matches 4; Conserv
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US-09-621-976-5605
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                                                                                                                                                                                                                                                                                                                                        US-09-252-991A-29933
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US-08-802-981-143
US-08-802-981-143
; Sequence 143, Application US/08802981
; Patent No. 60371-07
; Patent No. 60371-07
; PAPLICANT: Romoriya, Akira
; APPLICANT: Romoriya, Akira
; APPLICANT: Romoriya, Akira
; APPLICANT: Romoriya, Akira
; TITLE OF INVENTION: Compositions for the Detection of Enzyme
; TITLE OF INVENTION: Activity in Biological Samples and Methods of Use Thereof
; NUMBER OF SEQUENCES: 231
; CARRESPONDENCE ADDRESS:
; ADDRESSE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
STARE: California
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Indels
SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US/08/549,008
FILING DATE: 27-OCT-1995
CLASSIFICATION: 435
PRIOR APPLICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/802,981 FILING DATE: 20-FEB-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY AGENT INFORMATION:
NAME: Hunter, Tom
REGISTRATION NUMBER: 38,498
REFERENCE/DOCKET NUMBER: 016865-000300US
TELEPHONE: (415) 576-0200
TELEPHONE: (415) 576-0300
INFORMATION FOR SEQ ID NO: 143:
SEQUENCE CHARACTERISTICS:
LENGTH: 9 amino acids
                                                                                                                                                                                                                                                                                       32,762
FR: 016865-000110US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
                                                                                                                                                       CLASSIFICATION: 1.5.
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE: 28-OCT-1994
ATTORNEY/AGENT INFORMATION:
NAME: Weber, Ellen Lauver
REGISTRATION NUMBER: 32,762
REFERENCE/DOCKET NUMBER: 016865-000
TELECHONNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEPHONE: (415) 576-0300
JELEPHONE: (415) 576-0300
JENGTH: 9 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            64.3%;
50.0%;
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Best Local Similarity 50.0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-549-008-43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3 SVPLSVPC 10
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2 AIPMSIPC 9
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GENERAL INCOMPATION:
APPLICANT: Griffais, R.
TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments
TITLE OF INVENTION: thereof and uses thereof, in particular for the diagnosis, preve
TITLE OF INVENTION: and treatment of infection
FILE REFERENCE: 9710-003-999
CURRENT APPLICATION NUMBER: US/09/198,452A
CURRENT FILING DATE: 1998-11-24
NUMBER OF SEQ ID NOS: 6849
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
APPLICANT: MAKE O. Rubenfield et al.
APPLICANT: MAKE O. Rubenfield et al.
TITLE OF INVENTION: ARRUGINGS POR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: ARRUGINGS POR DIAGNOSTICS AND THERAPEUTICS
TITLE REFERENCE: 107195.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR FILING DATE: 1999-02-18
PRIOR FILING DATE: 1999-07-27
NUMBER OP SEQ ID NOS: 33142
SEQ ID NO 30161
LENGTH: 183
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Pred. No. 3.9e+02;
1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          h 62.5%; Score 35; DB 4; Length 183; Similarity 60.0%; Pred. No. 1.4e+02; 6; Conservative 1; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    62.5%; Score 35; DB 4; Length 201;
; CURRENT APPLICATION NUMBER: US/09/252,991A; CURRENT FILING DATE: 1999-02-18; PRIOR APPLICATION NUMBER: US 60/074,788; PRIOR FILING DATE: 1998-02-18; PRIOR FILING DATE: 1998-07-27; NUMBER OF SEQ ID NOS: 33142; SEQ ID NO 19384
                                                                                                                                                                                                                                                                                                                                             1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; Sequence 30161, Application US/09252991A; Patent No. 6551795
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            // Sequence 145, Application US/09198452A
// Patent No. 6559294
                                                                                                                                                                                                         TYPE: PRT
ORGANISM: Pseudomonas aeruginosa
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                                                                                                                                                                                                                                                                                                   64.3%;
                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 75.0.
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                                                                                                                                                                                                                                                                                                                                                                                                                                46 AAPLSVPC 53
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Matches 6; Conserv
                                                                                                                                                                                                                                                   US-09-252-991A-19384
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US-09-198-452A-145
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LENGTH: 201
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                                                                                                                           GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
APPLICANT: MOLLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS TITLE OF INVENTION: ABENGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US 60/074,788
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 29740
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS TITLE OF INVENTION: ABCUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US 60/074,788
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-07-108
PRIOR FILING DATE: 1998-07-27
NUMBER: OS 60/094,190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 19384, Application US/09252991A
Patent No. 6551795
ERNEAL IN. 6551795
APPLICANT:
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS TITLE OF INVENTION: ARRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 36; DB 4; Lengtn 3*1.
Pred. No. 1.98+02;
2; Indels
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Pred. No. 2.8e+02;
3; Mismatches 2; Indels
                                                                                     Sequence 29740, Application US/09252991A
Patent No. 6551795
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Patent No. 6551795
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           64.3%;
illarity 60.0%;
Conservative
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50.0%;
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Best Local Similarity 50.0
Matches 5; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
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US-09-252-991A-26663
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-09-252-991A-29740
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US-09-252-991A-19384
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LENGTH: 510
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Sequence 58, Application US/08722719
Patent No. 6001606
GENERAL INFORMATION:
APPLICANT: ROSEN, CRAIG A.
APPLICANT: ROSEN, TEVEN M.
APPLICANT: LI, HACDONG
I APPLICANT: ADAMS, MARK D.
ITILE OF INVENTION: THERAPEUTIC COMPOSITIONS AND METHODS FOR TITLE OF INVENTION: TREATING DISEASE STATES WITH MYELOID PROGENITOR INHIBITORY ITILE OF INVENTION: (M-CIF), AND MACROPHAGE INHIBITORY FACTOR.
ITILE OF INVENTION: (M-CIF), AND MACROPHAGE INHIBITORY FACTOR.
ITILE OF INVENTION: (M-CIF), AND MACROPHAGE INHIBITORY FACTOR.
ITILE OF INVENTION: (M-CIF), AND MACROPHAGE INHIBITORY FACTOR.
ITILE OF DADRESS: 64
CORRESPONDENCE ADDRESS: ADDR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ij
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                                               Gaps
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    Pred. No. 1.6e+02;
2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.: 1100 NEW YORK AVENUE, N.W., SUITE 600 WASHINGTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDIUM TYRE: FILOPY G18K

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/722,719

FILING DATE: 30-SEP-1996

CLASSIFICATION: 435

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/173,209

FILING DATE: 22-DEC-1993

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/208,339

FILING DATE: 08-MAR-1994

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/46,881

FILING DATE: 05-MAY-1995

PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US 08/465,682

FILING DATE: 06-JUN-1995

PRIOR APPLICATION NUMBER: US 08/468,775

FILING DATE: 06-JUN-1995

PILING DATE: 06-JUN-1995
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: STEFFE, ERIC K.
REGISTRATION VINDRER: 36,688
REFERENCE/DOCKET NUMBER: 1488.0330007
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEPHONE: (202) 371-2600
TELEPAX: (202) 371-250
INFORMATION FOR SEQ ID NO: 58:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        not relevant
62.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY: USA
ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          72 amino acids
Best Local Similarity 62.5
Matches 5; Conservative
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MOLECULE TYPE: protein
                                                                                                                                                                             |:|: |||
104 SIPVDVPC 111
                                                                                                                             3 SVPLSVPC 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-08-722-719-58
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Search completed: September 5, 2004, 10:22:01 Job time: 9.88889 secs
1 CIS-VPLSVPC 10
                   7 CISYTPRSIPC 17
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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OM protein - protein search, using sw model

5, 2004, 09:47:29; Search time 6.90909 Seconds (without alignments) 125.302 Million cell updates/sec September Run on:

US-09-761-636A-14 52 1 CISVPLVPC 9 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283366 segs, 96191526 residues Searched:

283366 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

PIR 78:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:* Database

......

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		de			SUMMARIES	
Result No.	Score	Query Match	Length	DB	ID	Description
1	39		l Q	0	L LO	hypothetical prot
01	39	75.0	347	~	A81988	probable N-acetyl
3	39		347	7	D81043	N-acetyl-gamma-gl
4	39	75.0	416	N	40	keratin A, type I
Ŋ	39		416	7	A46559	keratin, type I,
9	38	73.1	154	~1	D82795	phage-related end
7	38	73.1	577	7	T00416	hypothetical prot
œ	38	73.1	2	N	C84918	TP
δ	38	73.1	3623	~	T08618	intrinsic factor-
10	37	71.2	287	7	H64690	type IIS restrict
11	37	71.2	407	7	T19895	hypothetical prot
12	36		1639	7	T50119	probable sensory
13	35		61	N	JQ1086	nodulin-14 precur
14	35	67.3	278	7	AF0936	probable Arac-fam
15	35		305	~	A82728	conserved hypothe
16	35		496	7	S51668	tyrosine kinase -
17	35		21	7	D88013	protein K10B4.1
18	35	67.3	1440	П	SYHUQT	multifunctional a
19	35		24	~	T37057	probable multi-do
20	34	65.4	397	7	AC1877	hypothetical prot
21	34	65.4	551	~	JC7562	glioblastoma RING
22	34		1876	~1	T13801	phosphoinositide
23	33		3	~	AI3609	daunorubicin resi
24	33	63.5	370	7	T25627	hypothetical prot
25	33		m	7	T01390	
26	33		491	7	T46915	
27	33	63.5	σ	Н	S53834	О
28	33		498	~	4	acetate CoA-trans
29	33		(7	7	9	neural cell adhes

Thirthe and the control of the contr

probable cation tr	hypothetical prote	probable dehydroge	probable dehydroge	probable ribonucle	probable DNA-direc	prestalk protein p	structural polypro	cutl protein - fis	cutl protein - fis	lon protein - Esch	E5 protein - human	thrombospondin - b	probable inclusion	hypothetical prote	dual specificity p
F70757	A65072	B91098	F85943	T41246	S26985	A26838	VHWV	A35694	T41455	A23101	W5WL39	A61594	D71541	T02683	A47196
7	N	7	~	~	7	7	Н	~	~1	~	Н	N	7	7	П
771	926	926	926	957	1021	1046	1253	1827	1828	58	72	84	115	174	185
63.5	63.5	63.5	63.5	63.5	63.5	63.5	63.5	63.5	63.5	61.5	61.5	61.5	61.5	61.5	61.5
33	33	33	33	33	33	33	33	33	33	32	32	32	32	32	32
30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

RESULT 1	
T25817	
hypothetical protein K12D9.3 - Caenorhabditis elegans	
C,Species: Caenorhabditis elegans	
C,Date: 15-Oct-1999 #sequence revision 15-Oct-1999 #text change 15-Oct-1999	
C, Accession: T25817	
R,Graves, T.	
submitted to the EMBL Data Library, November 1996	
A, Description: The sequence of C. elegans cosmid K12D9.	
A; Reference number: Z20093	
A; Accession: T25817	
A;Status: preliminary; translated from GB/EMBL/DDBJ	
A; Molecule type: DNA	
A;Residues: 1-297 <gra></gra>	
A; Cross-references: EMBL:U80030; PIDN:AAB37600.1; GSPDB:GN00023; CESP:K12D9.3	۳.
A; Experimental source: strain Bristol N2; clone K12D9	
C;Genetics:	
A; Gene: CESP:K12D9.3	
A;Map position: 5	
A;Introns: 165/3; 208/3	
75.0%;	
cal Similarity 66.7%; Pred. No. 14;	,
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps C	٥؛
Qy 1 CISVPLVPC 9	
Db 169 CISLPIVIC 177	
C HILDRA	

A;Gene: argC; NMA0676 C;Superfamily: N-acetyl-gamma-glutamyl-phosphate reductase C;Keywords: oxidoreductase

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Gaps

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phage_related endolysin XF0513 [imported] - Xylella fastidiosa (strain 9a5c)
C;Species: Xylella fastidiosa
C;Species: Xylella fastidiosa
C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 23-Mar-2001
C;Accession: D87795
R;anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Sequen Nature 406, 151-157, 2000
A;Title: The genome sequence of the plant pathogen Xylella fastidiosa.
A;Reference number: A02515; MUID:20365717; PMID:.0910347
A;Note: for a complete list of authors see reference number A59328 below
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-154 <SINA
A; Residues: 1-154 <SINA
A; Residues: 1-154 <SINA
A; Residues: 1-154 <SINA
A; Cross-references: GB:AE003900; GB:AE003849; NID:g9105366; PIDN:AAF83323.1; GSPDB:GN001
A; Experimental source: strain 9a5c
A; Experimental source: strain 9a5c
R; Simpson, A.J.G.; Reinard, P.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.; Fsimson, M.R.; Buenco, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carrarc, D.M.; Carrer, B. as-Neto, E.; Docena, C.; El-Dorry, H.; Facincani, A.P.; Ferreira, A.J.S.
as-Neto, E.; Docena, C.; El-Dorry, H.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Frobm S; Authors: Ferreira, W.C.A.; Ferreira, H.M.F.; Marting, C.B.; Kuramae, B.E.; Laigrachdo, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Martins, C.L.; Mardeis, M.V.; Mattins, E.M.F.; Mattins, M.A.; de Oilveira, M.C.; de Oilveira, R.C.; Palmierit, D.F. Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sawash M.; Tsuhako, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.; A.L.; A.L.; A.L.; A.L.; Verjovski-Almeida, S.; Vettore, A.L.; A.L.; A.L.; A.L.; A.L.; Verjovski-Almeida, S.; Vettore, A.L.; A.L.; A.L.; A.L.; A.L.; A.L.; A.L.; Verjovski-Almeida, S.; Vettore, A.L.; 
J. Invest. Dermatol. 91, 541-546, 1988
A;Title: Cloning and characterization of a mouse type I hair keratin cDNA.
A;Reference number: A46559; MUID:89054860; PMID:2461417
A;Accession: A46559
A;Status: preliminary
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Residues: 1-416 < BER>
A;Cross-references: GB:M27734; NID:g198585; PIDN:AAA39372.1; PID:g198586
C;Superfamily: cytoskeletal keratin
                                                                                                                                                                                                                                                                                                                                                                                        Query Match 75.0%; Score 39; DB 2; Length 416; Best Local Similarity 66.7%; Pred. No. 19; Matches 6; Conservative 1; Mismatches 2; Indels
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Best Local Similarity 75.0%;
Matches 6; Conservative ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CVSNPCVPC 393
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 CISVPLVPC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Accession: D82795
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A.Gene: XF0513
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E/Accession: D81043

E/Authors Carnald, G.; Sun, L.; Smith, H.O.; Frasser, C.M.; Moxon, E.R.; Rappuoli, R.; Ve A; Reference number: A81000; MUID:20175755; PMID:10710307

A/Accession: D81043

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R;Kaytes, P.S.; McNab, A.R.; Rea, T.J.; Groppi, V.; Kawabe, T.T.; Buhl, A.E.; Bertolino, J. Invest. Dermatol. 97, 835-842, 1991
A;Title: Hair-specific keratins: characterization and expression of a mouse type I kerat A;Reference number: A61404; MUID: 92013235; PMID:1171610
                                                                                                                                                                                                                                                                                                                                                                                                                N-acetyl-gamma-glutamyl-phosphate reductase NMB1787 [imported] - Neisseria meningitidis
C;Species: Neisseria meningitidis
C;Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 19-Jan-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Cross-references: GB:AE002528; GB:AE002098; NID:g7227034; PIDN:AAF42126.1; PID:g722704
A;Experimental source: serogroup B, strain MC58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           keratin, type I, hair (clone MHXA-1) - mouse
C;Species: Mus musculus (house mouse)
C;Date: 01-Mar-1994 #sequence_revision 03-Mar-1994 #text_change 13-Aug-1999
C;Accession: A46559
R;Bertolino, A.P.; Checkla, D.M.; Notterman, R.; Sklaver, 1.; Schiff, T.A.; Freedberg,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
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A;Staus: preliminary; not compared with conceptual translation
A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-416. «KAY>
C;Superfamily: cytoskeletal keratin
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   Length 347;
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                                                                                   Indels
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Pred. No. 16;
2; Mismatches
Score 39; DB 2
Pred. No. 16;
2; Mismatches
75.0%;
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Best Local Similarity 75.v.
6; Conservative
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Best Local Similarity 66.7
Matches 6; Conservative
                                                                           6; Conservative
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156 CVSLPLVP 163
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CVSLPLVP 163
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                                       Similarity
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Query Match
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Matches 6
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hypothetical protein T30B22.1 - Arabidopsis thaliana (5.Species: Arabidopsis thaliana (mouse-ear cress) (5.Species: Arabidopsis thaliana (mouse-ear cress) (5.Date: 0.1-Feb-1999 #sequence_revision 01-Feb-1999 #text_change 24-Nov-1999 (5.Accession: T00416 R:R. (2.1. Februaley, S.D.; Lin, X.; Ketchum, K.A.; Crosby, M.L.; Brandon, R.C.; Sykes, S.M.; Masce Bubmitted to the BMBL Data Library, October 1998 A; Description: Arabidopsis thaliana chromosome II BAC T30B22 genomic sequence. A; Reference number: 214149
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                                                                                                                                                                        Gaps
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                                                                Score 38; DB 2; Length 154;
Pred. No. 11;
2; Mismatches 0; Indels
C, Superfamily: phage T4 lysozyme; phage T4 lysozyme homology
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5 10:36:26 2004

San Sep

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C; Accession: H64690
R; Tomb, J.F.; White, O.; Kerlavage, A.R.; Clayton, R.A.; Sutton, G.G.; Fleischmann, R.D. Peterson, S.; Loftus, B.; Richardson, D.; Dodson, R.; Khalak, H.G.; Glodek, A.; McKennel son, J.D.; Kelley, J.M.; Cotton, M.D.; Weidman, J.M.; Fujii, C.; Bowman, C.; Watthey, L. Nature 388, 539-547, 1997
A; Authors: Wallin, E.; Hayes, W.S.; Borodovsky, M.; Karpk, P.D.; Smith, H.O.; Fraser, C. A; Title: The complete genome sequence of the gastric pathogen Helicobacter pylori.
A; Reference number: A64520; MUID: 97394467; PMID: 9252185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Cross-references: GB:AE000637; GB:AE000511; NID:g2314536; PIDN:AAD08412.1; PID:g231453
Genetics:
A;Start codon: TTG
C;Superfamily: type II site-specific DNA-methyltransferase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 probable sensory transduction histidine kinase [imported] - fission yeast (Schizosacchar
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Status: preliminary; nucleic acid sequence not shown; translation not shown A;Molecule type: DNA A;Residues: 1-287 <TOM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-407 <WIL>
A;Cross-references: EMBL:Z81048; PIDN:CAB02841.1; GSPDB:GN00019; CESP:C41G7.4
A;Experimental source: clone C41G7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C,Species: Caenorhabditis elegans
C,Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
                                                                                                                                                                                                                                                                                                                                             type IIS restriction enzyme M2 protein - Helicobacter pylori (strain 26695)
C;Species: Helicobacter pylori
                                                                                                                                                                                                                                                                                                                                                                                                      C,Date: 09-Aug-1997 #sequence_revision 09-Aug-1997 #text_change 22-Jun-2003
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0
                        Length 3623;
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Pred. No. 31;
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                              Score 38; DB 2;
Pred. No. 2.3e+02;
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R,Steward, C.
submitted to the EMBL Data Library, October 1996
                                                                                    0; Mismatches
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A;Introns: 27/2; 107/3; 151/3; 333/3; 373/3
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75.0%;
                              73.18;
66.78;
                           Query Match 73.1
Best Local Similarity 66.7
Matches 6; Conservative
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A;Accession: T19895
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86 CINVPLMP 93
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Best Local Similarity
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Best Local Similarity
Matches 6; Conserv
                                                                                                                                              1 CISVPLVPC
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A;Gene: CESP:C41G7.4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 probable ATP-dependent RNA helicase A [imported] - Arabidopsis thaliana (Species: Arabidopsis thaliana (mouse-ear cress) (Jate: 02-Peb-2001 #sequence_revision 02-Peb-2001 #text_change 02-Peb-2001 (Jate: 02-Peb-2001 #sequence_revision 02-Peb-2001 #text_change 02-Peb-2001 (Jate: 02-Peb-2001 S.) Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.; R.Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, M.; VanAken, S.E.; Umayam, L.; Tallon, L. euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J. A.; Titles Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana. A;Accession: C84918
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R;Moestrup, S.K.; Kozyraki, R.; Kristiansen, M.; Kaysen, J.H.; Rasmussen, H.H.; Brault, J. Biol. Chem. 273, 5235-5242, 1998
A;Title: The intrinsic factor-vitamin B12 receptor and target of teratogenic antibodies A;Reference number: Z16459; MUID:98148073; PMID:9478979
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C;Keywords: egg yolk; endocytosis; glycoprotein; intestine; kidney; peripheral membrane
F;1-20/Domain: signal sequence #status predicted <SIG>
F;1-23/Droduct: intrinsic factor-B12 receptor CUBILIN #status predicted <MAT>
F;133-164/Domain: EGF homology <EGF1>
F;436-467/Domain: EGF homology <EGF>
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;Molecule type: mRMs
Fassidues: 1-3623 <MOE>
;Cross-references: EMBL:AF022247; NID:g3834379; PIDN:AAC71661.1; PID:g3834380
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A;Residues: 1-1015 <STO>
A;Cross-references: GB:AE002093; NID:g3738282; PIDN:AAC63624.1; GSPDB:GN00139
C;Genetics:
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C;Species: Rattus norvegicus (Norway rat)
C;Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 02-Aug-2002
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A,Introns: 87/3; 126/3; 175/1; 264/3; 329/3; 507/3
C,Superfamily: Arabidopsis thaliana hypothetical protein T30B22.1
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                                                                                                                                                                                                                                                                                                                     Score 38; DB 2; Length 577;
Pred. No. 40;
                                                                           A,Residues: 1-577 <ROU>
A,Cross-references: EMBL.AC002535; NID:g2529657; PID:g2529658
A,Experimental source: cultivar Columbia
C,Genetics:
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                        A;Status: translated from GB/EMBL/DDBJ
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75.0%;
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Best Local Similarity 75.0
Matches 6; Conservative
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Best Local Similarity
Matches 6; Conserv
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                                                      A, Molecule type: DNA
A; Accession: T00416
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A;Map position: 2
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Length 278 1; Indels

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A.Cross-references: GB:AL513382; PIDN:CAD09512.1; PID:g16504629; GSPDB:GN00176 Cydentelics: AT93756 C;Superfamily: hypothetical protein b2382
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Pred. No. 68;
2; Mismatches
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                                                                                                                                                          67.3%;
                                                                                                                                  4; Conservative
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Job time : 7.90909 secs
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56 ITAPLIPC 63
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Best Local Similarity
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SIPIIPC 9
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A;Molecule type: DNA
A;Residues: 1-305 <SIM>
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        A;Residues: 1-278 <PAR>
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A;Residues: 1-61 <8CH>
A;Cross-terneces: GB-545162; NID:g257036; PIDN:AAB23538.1; PID:g257037
A;Cross-terneces: root nodule
C;Comment: The gene encoding this protein is expressed in the second stage of root nodul
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R;Parkhill, J; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher, th, T.; Connerton, P.; Cronin, A.; Davies, R.M.; Dowd, L.; White, N.; Farrar, S.; Moule, S.; O'Gaora, P.

A; S.; Moule, S.; O'Gaora, P.

A; Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; A; Refreence number: AB0502; MUID:21534947; PMID:11677608
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C,Accession: JQ1086
R;Scheres, B:: van Eggelen, F:; van der Knaap, E:; van de Wiel, C:; van Kammen, A.; Bis Plant Cell 2, 687-700, 1990
A;Title: Sequential induction of nodulin gene expression in the developing pea nodule. A;Reference number: JQ1084; MUID:93005665; PMID:2152123
                                                                                                                                                                                A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-1639 <SBE
A;Residues: 1-1639 <SBE
A;Residues: BMBL:AL157734; PIDN:CAB75776.1; GSPDB:GN00066; SPDB:SPAC1834.08
A;Experimental source: strain 972h(-); cosmid c1834
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C;Species: Pisum sativum (garden pea)
C;Date: 23-Nov-1991 #sequence_revision 23-Nov-1991 #text_change 20-Apr-2001
C;Species: Schizosaccharomyces pombe
C;Date: 09-Jun-2000 #sequence_revision 09-Jun-2000 #text_change 09-Jun-2000
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                                                              R;Seeger, K.; Harris, D.; Wood, V.; Rajandream, M.A.; Barrell, B.G. submitted to the EMBL Data Library, February 2000
A;Reference number: Z25039
A;Accession: T50119
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 1639;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 67.3%; Score 35; DB 2; Length 61; Best Local Similarity 71.4%; Pred. No. 16; Matches 5; Conservative 2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 36; DB 2; Length 163
Pred. No. 2.5e+02;
1; Mismatches 0; Indels
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F;1-20/Domain: signal sequence #status predicted <SIG>F;21-61/Product: nodulin 14 #status predicted <MAT>
                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 85.7%;
Matches 6; Conservative
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NIPLVPC 27
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A;Molecule type: DNA
                                                      Accession: T50119
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A; Introns: 23/3
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Conserved hypothetical protein XF1068 [imported] - Xylella fastidiosa (strain 9aSc) C;Species: Xylella fastidiosa C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 20-Aug-2000 C;Datesion: A82728  
R;Anconymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Sequer Nature 406, 151-157, 2000 A;Fitle: The genome sequence of the plant pathogen Xylella fastidiosa. A;Reference number: A82515; MUD:20365717; PMID:10910347 A;Reference number A82728 A;Accession: A82728
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;CESS-references: GB:AE003943; GB:AE003849; NID:g9106006; PIDN:AAF83878.1; GSPDB:GN001A;CSS-references: strain 9aSc
A;Experimental source: strain 9aSc
A;Experimental source: strain 9aSc
A;Eximpson, A.JG: Reinard, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.; P. Briones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carrer, Ass.Neto, E.; Docena, C.; El-Dorry, H.; Facincani, A.P.; Ferreira, A.J.S.
as-Neto, E.; Docena, C.; El-Dorry, H.; Facincani, A.P.; Ferreira, A.J.S.
A;Authors: Perreira, V.C.A.; Ferro, J.A.; Franca, S.C.; Franco, M.C.; Frohm J.D.; Unqueira, M.L.; Kemper, E.L.; Kttajima, J.P.; Krieger, J.E.; Kuramae, E.E.; Laign-Chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Marino, C.L.; Marques, M.V.; Martins, E.M.F.; Marsukuma, A.Y.; Marino, C.L.; Marques, W.V.; Martins, E.M.F.; Marsukuma, A.Y.; Marino, C.L.; Marques, W.V.; Martins, E.M.P.; Marsukuma, A.Y.; Marino, C.L.; Marques, M.V.; Martins, E.M.P.; Martins, Mart
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Pred. No. 74;
3; Mismatches 0; Indels
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57.1%; Pred. No.
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OM protein - protein search, using sw model

September 5, 2004, 09:38:39 ; Search time 4.09091 Seconds (without alignments)
114.554 Million cell updates/sec Run on:

US-09-761-636A-14 52 1 CISVPLVPC 9 Title: Perfect score: Sequence: BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

141681 seqs, 52070155 residues Searched:

141681 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt_42:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description			ners	mus ma	P26415 pisum sativ	human	cucump	_		075751 homo sapien	mycob		homod	mus m	bra		xenor				escherichi	P33537 neurospora			P18296 schizosacch							154		escher
SUMMARIES	qı		ANGC NEIMA	ARGC NEIMB	KIMI_MOUSE	NOI4_PEA		MOVP_CMVAS		1 1	OCN3_HUMAN	EMBA_MYCAV	SYEP HUMAN	RN27 HUMAN	RN27 MOUSE	BBS2_BRARE	M172 HUMAN	TSP1 XENLA	NU4M_ACACA	CTPG_MYCTU	XDHD_ECO57	XDHD_ECOLI	DPOM_NEUCR	PSTA_DICDI	POLS_SFV	CUT1_SCHPO		٠,	AROK SYNEL	DUS3_HUMAN	DUS3 MOUSE	PLC1 CAEEL	CORA HPBDU	NRT1 CHICK	GATD_ECOLI
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DHB2_HUMAN	GAT1 RAT	RSP6_CHLRE	KIM6 HUMAN	ACSA_VIBCH	T9S2 MOUSE	T9S2 HUMAN	DD20 HUMAN	TSP1 BOVIN	TSP1 HUMAN	TSP1_MOUSE
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387	413	459	467	649	662	663	824	1170	1170	1170
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32	35	32	32	32	32	32	32	32	32	32
34 7.	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

Query Match

DB 1; Length 347; 75.0%; Score 39;

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KIM1 MOUSE
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                                                                                                             061765;
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KIM1_MOUSE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright, It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@18b-sib.ch).
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MEDLINE-2017575; PubMed=10710307;
Bisen J.A., Ketchum K.A., Heidelberg J., Jeffries A.C., Nelson K.E., Eisen J.A., Ketchum K.A., Hood D.W., Peden J.F., Dodson R.J., Nelson W.C., Gwinn M.L., DeBoy R., Peterson J.D., Hickey E.K., Malon W.C., Gwinn M.L., DeBoy R., Peterson J.D., Hickey E.K., Mason T., Ciecko A., Parksey D.S., Blair E., Cittone H., Clark B.B., Cotton M.D., Utterback T.R., Khouri H., Qin H., Vamathevan J., Scarlato V., Masignan Y., Pizza M., Grandi G., Sun L., Smith H.O., Fraser C.M., Moxon E.K., Rappuoli R., Venter J.C., "Complete genome sequence of Neisseria meningitidis serogroup B strain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -i- CATALYTIC ACTIVITY: N-acetyl-L-glutamate 5-semialdehyde + NADP(+) + phosphate = N-acetyl-5-glutamyl phosphate + NADFH.
-i- PATHWAY: Arginine biosynthesis; third step.
-i- SUBCELLULA. LCCATION: Cytoplasmic (Probable).
-i- SUBCELLULA. Belongs to the NAGSA dehydrogenase family. Subfamily
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                     Gaps
                                                                                                                                                                                                                                                                                                    28-FZB-2003 (Rel. 41, Last sequence update)
10-607-2003 (Rel. 42, Last annotation update)
10-cortyl-gamma-glutamyl-phosphate reductase (EC 1.2.1.38) (AGPR) (N-acetyl-glutamate semialdehyde dehydrogenase) (NAGSA dehydrogenase).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TIGR; NMB.100/; -. 1.

HAMAP; MF 00150, -; 1.

InterPro; IPR000706; AGPR act site.

InterPro; IPR000534; Semialdh_dh.

Pfam; PF021118; Semialdhyde_dh; 1.

Pfam; PF02174; Semialdhyde_dh; 1.

Procon; P00376; AGRR act site; 1.

PROSITE; PS01224; ARGC; FALSE NBG.

Arginine biosynthesis; Oxidoreductase; NADP; Complete proteome.

152 BY SILLARITY.
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                                                                                                                                                                                                                                                                                                                                                                                                                         Neisseria meningitidis (serogroup B).
Bacteria, Proteobacteria, Betaproteobacteria, Neisseriales,
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Pred. No. 4.2;
2; Mismatches (
  Pred. No. 4.2;
                                                                                                                                                                                                                                     347 AA
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                                                                                                                                                                                                                                                                                   (Rel. 41, Created)
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75.0%;
75.0%;
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                          6; Conservative
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156 CVSLPLVP 163
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Best Local Similarity
6, Conserve
                                                                      1 CISVPLVP 8
    Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                       ARGC NEIMB
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                          Matches
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156 CVSLPLVP 163

1 CISVPLVP 8

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration
                                                                                                                                                                                                                                                                                                                                                                        J. Invest. Dermatol. 91:541-546(1988).

-!- MISCELLANEOUS: THERE ARE TWO TYPES OF HAIR/MICROFIBRILLAR KERATIN, I (ACIDIC) AND II (NEUTRAL TO BASIC).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
STRAIN=C57BL/6J; TISSUB-Hair;
MEDLINE=89054860; PubMed=2461417;
Bertolino A.P., Checkla D.M., Notterman R., Sklaver I., Schiff T.A.,
Bertolino A.P., Chdona G.J.;
"Cloning and characterization of a mouse type I hair keratin cDNA.";
                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
                                   15-UUL-1998 (Rel. 36, Created)
15-UUL-1998 (Rel. 36, Last sequence update)
16-UT-2001 (Rel. 40, Last annotation update)
Keratin, type I cuticular HAI (Hair keratin, type I HAI) (HKA-1).
KRTHAI OR KRTI-1 OR HKAI.
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COIL 2.
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COIL 1A.
LINKER 1.
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InterPro; IPR001664; IF.
InterPro; IPR002957; Keratin_I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRINTS; PRO1248; TYPE1KERATIN.
PROSITE; PS00226; IF; 1.
Intermediate filament; Colled
DOMAIN 2 56 H
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Best Local Similarity 66.7
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pfam; PF00038; filament;
STANDARD;
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102
203
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364
92
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416 AA;
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EMBL, U21941; AAC54855.1; -.
InterPro; IPR004270; Papilloma_E5.
Pfam; PF03025; Papilloma_E5; 1.
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InterPror; IRRO00603; 3A mov.
Pfam; PF00603; 3A; 1.
DNA-binding; Transport.
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15-DEC-1998 (Rel. 37, Last sequ
15-DEC-1998 (Rel. 37, Last anno
                                                                                              67.3%;
                                                                     9262 MW;
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Matches 6; Conserv
                                                                                                            Similarity
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                                                                     78 AA;
                                                                                                                                                   1 CISVPLVP
                                                                                                                                                                                  CCSVPLLP
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                                                      Early protein SEQUENCE 78
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Matches
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                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation—the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                        -!- MISCELLANEOUS: CONTAINS 4 CYSTEINES ARRANGED IN TWO PAIRS IN SUCH
A WAY THAT THEY MIGHT BE CAPABLE OF BINDING A METAL ION.
-!- SIMILARITY: TO NODULIN 3.
                                                                                                                                                                                             -!- DEVELOPMENTAL STAGE: Expressed in the second stage of root nodule
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
           Eukaryota; Viridiplantãe; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Vicieae; Pisum.
                                                                                         STRAIN=CV. Sparkle, TISSUB=Root nodules, MEDLINE=99005665; PubMed=2152123; MEDLINE=99005665; PubMed=2152123; MEDLINE=99005665; PubMed=2152123; MEDLINE=9905665; PubMed=2152123; Van der Knaap E., van de Wiel C., van Kammen A., Bisseling T.; "Sequential induction of nodulin gene expression in the developing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=96249586; PubMed=8815087;
Forslund O., Hansson B.G.;
"Human papillomavirus type 70 genome cloned from overlapping PCR
products: complete nuclectide sequence and genomic organization.";
J. Clin. Microbiol. 34:802-809(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .;
0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human papillomavirus type 70.
Viruses, dsDNA viruses, no RNA stage; Papillomaviridae;
Papillomavirus.
NCBI_TaxID=39457;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 D508059695F62B8B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
Probable ES protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    78 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     POTENTIAL.
NODULIN 14.
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PIR; JQ1086; JQ1086.
Nodulation; Signal; Metal-binding.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            71.48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              67.38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              7175 MW;
                                                                                                                                                                 nodule.";
nt Cell 2:687-700(1990)
Pisum sativum (Garden pea)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best_Local Similarity 71.4
Matches 5; Conservative
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21 NIPLVPC 27
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                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 AA;
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                                                      NCBI_TaxID=3888;
                                                                                                                                                                                                              formation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VES HPV70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE
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SIGNAL
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                                                                                                                                                                                  Plant
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                                                                                                                                            Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -!- SIMILARITY: Belongs to the cucumoviruses/bromoviruses 3A family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Kim S.H., Park Y.I.;
Submitted (JuL-1997) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: INVOLVED IN TRANSPORT OF THE VIRUS FROM THE INITIALLY
INFECTED CELLS TO ADJACENT CELLS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Cucumber mosaic virus (strain As) (CMV).
Viruses; ssRNA positive-strand viruses, no DNA stage; Bromoviridae;
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Bukaryota: Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Lagomorpha; Leporidae; Oryctolagus.
NCBI TaxID=9986;
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15-DEC-1998 (Rel. 37, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Coagulation factor X precursor (EC 3.4.21.6) (Stuart factor)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                67.3%; Score 35; DB 1; Length 279;
66.7%; Pred. No. 19;
Live 1; Mismatches 2; Indels
                                                                  Score 35; DB 1; Length 78; Pred. No. 5.2;
                                                                                                                                        1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 30509 MW; 2B47059288DC1069 CRC64;
DFEA59CB355042D1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Cell-to-cell movement protein (MP) (3A protein)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   279 AA
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                                                                                                                                        1; Mismatches
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Rattus.
             BGF-LIKE 1, CALCIUM-BINDING (POTENTIAL).
EGF-LIKE 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HYDROXYLATION (BY SIMILARITY).
CHARGE RELAY SYSTEM.
CHARGE RELAY SYSTEM.
CHARGE RELAY SYSTEM.
CHARGE RELAY SYSTEM.
BY SIMILARITY.
BY SIMILARI
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28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Organic cation transporter 3 (Solute carrier family 22, member 3).
SLC22A3 OR OCT3.
Rattus norvegicus (Rat).
ACTIVATED FACTOR XA, HEAVY CHAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          SIMILARITY).
GAMMA-CARBOXYGLUTAMIC ACID (BY
                                                                        GAMMA-CARBOXYGLUTAMIC ACID (BY
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                                                                                                          GAMMA-CARBOXYGLUTAMIC ACID
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GAMMA-CARBOXYGLUTAMIC ACID
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GAMMA-CARBOXYGLUTAMIC ACID
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                                                       SERINE PROTEASE
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0; Mismatches
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3274
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1121
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490 AA;
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Best Local Similarity
Matches 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=10116;
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233
86
125
233
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088446;
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CARBOHYD
SEQUENCE
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MEDINE-9726311; PubMed=9101642;

Redurthi U.R., Anderson K.D., James H.L.;

Pendurthi U.R., Anderson K.D., James H.L.;

Thromb. Res. 85:503-514(1997).

Thromb. Res. 85:503-514(1997).

I. FUNCTION: Reactor Xa is a vitamin K-dependent glycoprotein that converts prothrombin to thrombin in the presence of factor Va, calcium and phospholipid during blood clotting.

I. CATALITY CATIVITY: Preferential cleavage: Arg-| Thr and then Arg-|-11e bonds in prochrombin to form thrombin.

SUBUNIT: The two chains are formed from a single-chain precursor by the excision of two Arg residues and are held together by 1 or more disulfide bonds.

C. PIM: The vitamin K-dependent, enzymatic carboxylation of some converted and provided protein to bind calcium (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the SWiss Institute of Bioinformatics and the EMBL outstation - the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Glycoprotein; Hydrolase; Zerine protease; Plasma; Blood coagulation; Gamma-carboxyglutamic acid; Hydroxylation; Calcium-binding; Vitamin K; Signal; Zymogen; EGF-like domain; Repeat.
                                                                                                                                                                                                                                                                                                   -!-PTM: N- and O-glycosylated (By similarity).
-!-PTM: THE ACTIVATION PEPTIDE IS CLEAVED BY FACTOR IXA (IN THE INTRINSIC PATHWAY), OR BY FACTOR VIIA (IN THE EXTRINSIC PATHWAY)
(BY SIMILARITY).
-!-MISCELLANBOUS: Calcium also binds, with stronger affinity to another site, beyond the GLA domain.
-!-SIMILARITY: Belongs to peptidase family S1.
-!-SIMILARITY: Contains 2 EGF-like domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BY SIMILARITY.
FACTOR X LIGHT CHAIN.
FACTOR X HEAVY CHAIN.
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PROSITE; PS000010; ASX HYDROXYL; 1.
PROSITE; PS000012; EGF 2; 1.
PROSITE; PS50002; EGF 3; 1.
PROSITE; PS50002; EGF 3; 1.
PROSITE; PS01187; EGF 2; 1.
PROSITE; PS01187; EGF 2; 1.
PROSITE; PS01011; GLU_CARBOXYLATION; 1.
PROSITE; PS50204; TRYPEIN DOM; 1.
PROSITE; PS00134; TRYPEIN JI.
PROSITE; PS00135; TRYPEIN JI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; SU11.20, 1.
InterPro; IPR000152; Asx hydroxyl S.
InterPro; IPR000003; Cyg_Ser_trypsin.
InterPro; IPR001043; EGF_2.
InterPro; IPR00183; EGF_1I.
InterPro; IPR001843; EGF_1I.
InterPro; IPR001243; EGF_1I.
InterPro; IPR001244; Peptidase_SI.
InterPro; IPR001244; Peptidase_SIA.
InterPro; IPR001244; Peptidase_SIA.
InterPro; IPR001244; Peptidase_SIA.
InterPro; IPR001244; Vitk_dep_GIA.
Pfam; Pr00089; EGF; 2.
Pfam; Pr00089; LTYPBin; 1.
PRINTS; PR00010; GTRMCTRYPSIN.
PRINTS; PR00010; GTRMCTRYPSIN.
PRINTS; PR00010; GTRMCTRYPSIN.
PRINTS; SN00010; GTRMCTRYPSIN.
SMART; SN000179; EGF_CA; 1.
SMART; SN000069; GTA; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      POTENTIAL
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                                                                                                                                                                                                                                                                                            similarity)
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PROPEP
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(BY (BY (BY (BY (BY (BY (BY o,

Gaps

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556 AA

STANDARD;

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MEDLINE=99134299; PubMed=9933568;
Verhaagh S., Schweifer N., Barlow D.P., Zwart R.;
"Cloning of the mouse and human solute carrier 22a3 (Slc22a3/SLC22A3)
identifies a conserved cluster of three organic cation transporters on
mouse chromosome 17 and human 6q26-q27.";
Genomics 55:209-218 (1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=20425388; PubMed=10966924; Wu X., Huang W., Ganapathy M.E., Wang H., Kekuda R., Conway S.J., Leibach F.H., Ganapathy V.; Structure, function, and regional distribution of the organic cation transporter OCT3 in the kidney.";
                             075751; Q9UP02;
28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Organic cation transporter 3 (Extraneuronal monoamine transporter)
(EMT) (Solute carrier family 22, member 3).
                                                                                                                                                                                                       Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                              Gruendemann D., Schechinger B., Rappold G.A., Schoemig E., "Molecular identification of the corticosterone-sensitive extraneuronal catecholamine transporter.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE OF 513-556 FROM N.A., AND TISSUE SPECIFICITY.
                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A., FUNCTION, AND TISSUE SPECIFICITY
                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=99212254; PubMed=10196521;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nat. Neurosci. 1:349-351(1998).
                                                                                                                                                                                                                                                                             NCBI_TaxID=9606;
                                                                                                                                                                                   SLC22A3 OR EMTH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FUNCTION, AND 1
TISSUE=Kidney;
            TISSUE-Placenta;

TISSUE-Placenta;

M. T.S. V. Sebuda B. Dubmed=9830022;

M. X., Kekuda R., Huang W., Fei Y.-J., Leibach F.H., Chen J.,

A. Conway S.J., Ganapathy V.;

Tidentity of the organic cation transporter OCT3 as the extraneuronal monoamine transporter (uptake2) and evidence for the expression of the transporter in the brain.";

The transporter in the brain.";

J. Biol., Chem. 273:32776-32786(1998).

- FUNCTION: Mediates potential-dependent transport of a variety of organic cations. May play a significant role in the disposition of cationic neurotoxins and neurotransmitters in the brain.

- SUBCELLOUAR LOCATION: Integral membrane protein.

- SUBCELLOUAR LOCATION: Integral membrane protein.

- ITISSUE SPECIFICITY: HIGHLY EXPRESSED IN PLACENTA WITH MODERATE EXPRESSED, ESPECIALLY IN HIGHLY EXPRESSED.

EXPRESSED, ESPECIALLY IN HIPPOCAMPUS, CEREBELLUM AND CEREBRAL

- CORTEX. EXPRESSION IS LOW IN KIDNEY AND LUNG AND UNDETECTABLE IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its mose by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                "Cloning and functional characterization of a potential-sensitive, polyspecific organic cation transporter (OCT3) most abundantly expressed in placenta.";
       Kekuda R., Prasad P.D., Wu X., Wang H., Fei Y.-J., Leibach F.H., Ganapathy V.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SIMILARITY: Belongs to the sugar transporter family. Organic cation subfamily.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (POTENTIAL) . (POTENTIAL) . (POTENTIAL) .
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; AF055286; AAC40150.1; -...
InterPro: IPR00714; MFS.
InterPro: IPR004749; Organt transp.
InterPro: IPR0047818; Sub_transporter.
InterPro: IPR005829; Sub_transporter.
InterPro: IPR005829; Sug_transporter.
InterPro: IPR005829; Sug_transporter.
ITGRAMS; TIGR00899; 2A0119; 1.
PROSITE: PS00216; SUGAR_TRANSPORT_1; 1.
PROSITE: PS00216; SUGAR_TRANSPORT_2; FALSE NEG.
Transport: Ion transport; Transmembrane; Glycoprotein.
TRANSMEM 21 41.
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                                                                                                                                         Biol. Chem. 273:15971-15979(1998)
MEDLINE=98298098; PubMed=9632645;
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AND TISSUE SPECIFICITY.

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transporter OCT3 in the kidney.";

4m. J. Physiol. 279:F449-F458(2000).

-!- FUNCTION: Mediates potential-dependent transport of a variety of organic cations. May play a significant role in the disposition of cationic neurotoxins and neurotransmitters in the brain.

-!- SUBCELIOLAR LOCATION: Integral membrane protein.

-! TISSUB SPECIFICITY: EXPRESSED IN PLACENTA, SKELETAL MUSCIE, PROSTATE, AORTA, LIVER, FETAL LUNG, SALIVARY GLAND, ADERRAL STANDEY AND BRAIN CORPERS. NO EXPRESSION DETECTED IN SPLEEN.

-!- SIMILARITY: Belongs to the sugar transporter family. Organic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GO; GO:0005887; C:integral to plasma membrane; TAS.
GO; GO:0005624; C:membrane fraction; TAS.
GO; GO:0015101; F:organic cation transporter activity; TAS.
GO; GO:0015695; P:organic cation transport; TAS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PROSITE; PS00216; SUGAR TRANSPORT 1; 1.
PROSITE; PS00217; SUGAR TRANSPORT 2; FALSE NEG.
Transport; Ion transport; Transmembrane; Glycoprotein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR004749; Orgcat transp.
InterPro; IPR005828; Sub_transporter.
InterPro; IPR005829; Sug_transporter.
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TIGRFAMs; TIGR00898; 2A0119; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; AJ001417; CAA04751.1; -. EMBL; AF078749; AAD20977.1; -.
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PROSITE; PS50850; MFS; 1
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Gaps

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1; Indels

0; Mismatches

6; Conservative

Matches

116 SAPLVPC 122

RESULT 9 OCN3_HUMAN

3 SVPLVPC 9

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EMBL; X54326; CAA38224.1; -.
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0
                                                                                                                                                                                                                                                                                                                                                                                                                transferase involved in cell wall arabinan biosynthesis that is the target for the antimycobacterial drug ethambutol.";
Proc. Natl. Acad. Sci. U.S.A. 93:11919-11924(1996).
-!- FUNCTION: Arabinosyl transferase responsible for the polymerization of arabinose into the arabina of arabinosal arabinose into the arabina of arabinosal sci. SUBCELLULAR LOCATION: Integral membrane protein (Probable).
-!- SIMILARITY: BELONGS TO THE EMB FAMILY.
                                                                                                                                                   Gaps
                             POTENTIAL.
POTENTIAL.
POTENTIAL.
POTENTIAL.
N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                    Belanger A.E., Besra G.S., Ford M.E., Mikusova K., Belisle J.T., Brennan P.J., Inamine J.M.;
                                                                                                   (POTENTIAL)
                                                                                                                                                   .;
0
                                                                                                                                                                                                                                                                                                                   Bacteria, Actinobacteria, Actinobacteridae, Actinomycetales,
Corynebacterineae, Mycobacteriaceae, Mycobacterium.
                                                                                                                                                                                                                                                                                                                                                                                                            embAB genes of Mycobacterium avium encode an arabinosyl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR007680; Arab transf.
Pfam; PF04602; arab transf; 1.
Transferase; Glycosyltransferase; Transmembrane; Cell wall;
                                                                                                                            Score 35; DB 1; Length 556;
Pred. No. 40;
                                                                                                             C3CA2D77DD21C658 CRC64;
                                                                                                                                                                                                                                                           28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Probable arabinosyltransferase A (EC 2.4.2.-)
                                                                                                    (GLCNAC
                                                                                                                                                                                                                                        PRT; 1108 AA.
                                                                                                                                                   0; Mismatches
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                                                                                                    N-LINKED
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MEDLINE=97030297; PubMed=8876238;
                                                                                                              61279 MW;
                                                                                                                               67.3%;
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                                                                                                                                                    6; Conservative
                                                                                                                                                                                                                                          STANDARD;
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                                                                                                                                                                                         121 SAPLVPC 127
                                                                                                                                                                                                                                                                                                              Mycobacterium avium.
                                                                                                              556 AA;
                                                                                                                                                                      3 SVPLVPC 9
                                                                                                                                Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=1764;
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P71485;
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X MEDLINE-8826251; PubMed=3290852;
A Thoemmes P., Fett R., Schray B., Kunze N., Knippers R.;
Thoemmes P., Fett R., Schray B., Kunze N., Knippers R.;
Thoemce P., Fett R., Schray B., Kunze N., Knippers R.;
The Escherichia coli and yeast enzymes.";
Nucleic Acids Res. 16:5391-5406(1988).

I. CATALYTIC ACTIVITY: ATP + L-glutamate + tRNA(Glu) = AMP + diphosphate + L-glutamy1-tRNA(Glu).

C -1- CATALYTIC ACTIVITY: ATP + L-proline + tRNA(Pro) = AMP + diphosphate + L-proly1-tRNA(Glu).

C -1- CATALYTIC ACTIVITY: ATP + L-proline + tRNA(Pro) = AMP + Glutamy1-tRNA(Fro)                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -!- CAUTION: Ref.2 sequence differs from that shown due to a number of
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J. Biol. Chem. 266:1448-1455(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-M3T-1998 (Rel. 08, Created)
01-M3T-1992 (Rel. 22, Last sequence update)
10-0CT-2003 (Rel. 42, Last annotation update)
11-0CT-2003 (Rel. 42, Last annotation update)
12-0CT-2003 (Rel. 42, Last annotation update)
13-0CT-2003 (Rel. 42, Last annotation update)
14-0CT-2003 (Rel. 42, Last annotation update)
15-0CT-2003 (Rel. 42, Last annotation update)
16-0CT-2003 (Rel. 42, Last annotation update)
17-0CT-2003 (Rel. 42, Last annotation update)
17-0CT-2003 (Rel. 42, Last annotation update)
18-0CT-2003 (Rel. 42, Last annotation u
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-!- SIMILARITY: IN THE C-TERMINAL SECTION; BELONGS TO CLASS-II AMINOACYL-TRNA SYNTHETASE FAMILY.
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-!- CAUTION: Was originally thought to be a glutaminyl-tRNA
                                                                                                                                                                                                                                                                                                                                                        Score 35; DB 1; Length 1108; Pred. No. 81; Mismatches 0; Indels
       616 638 POTENTIAL.
653 675 POTENTIAL.
696 718 POTENTIAL.
1108 Aa, 117404 MW; OEDBE648768075FA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT; 1440 AA.
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MEDLINE=91107633; PubMed=1988429;
Fett R., Knippers R.;
                                                                                                                                                                                                                                                                                                                                                                               67.3%;
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28 CLAVPLLP 35
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Biochem.
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       ö
                                                                                                                                                                                                                                                  TIGRFAMS; TIGRO0463; GltX arch; 1.
TIGREAMS; TIGRO0408; pros_fam 1; 1.
PROSITE; PSCO178; AA TRNA_LIGASE_1; 1.
PROSITE; PSCO862; AA TRNA_LIGASE_11; 1.
PROSITE; PSCO762; WHEP_TRS; 3.
Aminoacy1-tRNA synthetase; Protein biosynthesis; Ligase; ATP-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     098ZR9; 09C028;
16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
(Tripartite motif-containing protein 8).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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0
                                                                                                                                                                                                                                                                                                                               3 X 57 AA APPROXIMATE REPEATS.
PROLYI-TRNA SYNTHETASE.
"HIGH" REGION.
"KMSKS" REGION.
ATP (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 1440;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                      MW; C4E185A0AA41C204 CRC64;
                                                                                                                                                                                                                                                                                                             Multifunctional enzyme; Repeat; 3D-structure.
DOMAIN 92 687 GLUTAMYL-TRNA SYNTHETASE.
                                        MIM' 138295; -.

QO; GO:00054237; C:cytoplasm; TAS.

GO; GO:0005424; C:soluble fraction; TAS.

GO; GO:0005461; P:protein complex assembly; TAS.

InterPro; IPR004026; Gltx arch.

InterPro; IPR004046; GST_Cterm.

InterPro; IPR004184; HGTP anticodon.

InterPro; IPR004184; HGTP anticodon.

InterPro; IPR004199; ProS_fam I.

InterPro; IPR004199; ProS_fam I.

InterPro; IPR001114; tRNA-Synt_I.

InterPro; IPR001112; tRNA-Synt_I.

InterPro; IPR001112; tRNA-Synt_I.

InterPro; IPR00118; tRNA-Synt_I.

InterPro; IPR00198; MHEP-TRS.

Pfam; PF03129; TRNA-Synt_I.

Pfam; PF03129; TRNA-Synt_I.

Pfam; PF00489; MHEP-TRS.

PFam; PF00489; MHEP-TRS.

PRINTS; PR00489; TRNA-SYNTHGIU.

PRINTS; PR01086; TRNA-SYNTHGIU.

PRINTS; PR01086; TRNASYNTHGIU.

PRINTS; PR01086; TRNASYNTHGIU.

PRINTS; PR01086; TRNASYNTHGIU.
                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 35; DB 1; I
Pred. No. 1.1e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                               WHEP-TRS 1.
WHEP-TRS 2.
WHEP-TRS 3.
CHARGED.
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MEDLINE=20568703; PubMed=11118312;
Vincent S.R., Kwasnicka D.A., Fretier P.;
  EMBL; X07466; CAA30354.1; ALT SEQ
                                                                                                                                                                                                                                                                                                                                                                                                                      163026
                                                                                                                                                                                                                                                                                                                                                                                                                                                 44.48;
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es 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
         PIR; A38663; SYHUQT.
PDB; 1FYJ; 31-DEC-02.
Genew; HGNC:3418; EPRS.
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                                                                                                                                                                                                                                                                                                                                                                                                                      1440 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
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132
360
363
688
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                                       MIM; 138295; -.
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RI Blochem Bloophys Res. Commun. 279:482-486 (2000).

RE Blochem Bloophys Res. Commun. 279:482-486 (2000).

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BRARE
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ZN_FING
DOMAIN
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 15
M172_HUMAN
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BBSZ_BRARE
ID _BBSZ_BI
                                                                                                             Matches
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         STATES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  -1-SUBUNIT: Homodinier (By similarity).
-1-SUBUNIT: Homodiner (By similarity).
-1-SUBUNIT: Homodiner (By similarity).
-1-SUBCELLUIAR LOCATION: Nuclear (By similarity).
-1-DEVELOMENTAL STAGE: At 10.5 and 12.5 dpc, expressed in the central nervous system. At 14.5 dpc, expressed in the eye (lens and inner neural layer of the retina), in the primitive glomeruli of the developing kidney, in the villi of the gut and in the dorsal root ganglia.
-1-DOMAIN: The coiled coil domain is required for homodimerization (By similarity).
                                Gaps
                                                                                                                                               099572; 099p04;
16-0CT-2001 (Rel. 40, Created)
16-0CT-2001 (Rel. 40, Last sequence update)
16-0CT-2003 (Rel. 42, Last annotation update)
RING finger protein 27 (Glioblastoma-expressed ring finger protein)
(Tripartite motif protein 8).
                                                                                                                                                                                                                                        Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE OF 196-463 FROM N.A.
MEDILINE=21231161, PubMed=11331580,
MEDILINE=21231161, PubMed=11331580,
Reymond A., Merconi G., Fantozzi A., Merla G., Cairo S., Luzi L.,
Riganelli D., Zanaria E., Messali S., Cainarca S., Guffanti A.,
Minucci S., Pellicci P.G., Ballabio A.;
"The tripartite morif family identifies cell compartments.";
EMBO J. 20:2140-2151(2001).
                                ô
          DB 1; Length 551;
                               1; Indels
                                                                                                                                                                                                                                                                                                   TISSUE=Brain;
MEDILINE=20568703; PubMed=11118312;
Vincent S.R.; Kwasnicka D.A., Fretier P.;
"A novel RING finger-B box-coiled-coil protein, GERP.";
Biochem. Biophys. Res. Commun. 279:482-486 (2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -!- SIMILARITY: Contains 1 RING-type zinc finger.
                                                                                                                                       551 AA
                    Pred. No. 61;
0; Mismatches
            Score 34;
            65.4%;
85.7%;
Query Match
Best Local Similarity B5...
6. Conservative
                                                                                                                                       STANDARD;
                                                                             361 SVPLYPC 367
                                                                                                                                                                                                                                 Mus musculus (Mouse)
                                                       3 SVPLVPC 9
                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
Cyprinidae; Danio.
NCBI_TaxID=7955;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            M172 HUMAN STANDARD; Q96GB6; Q9NRF7; 966 AA. Q14596; Q13173; Q1526; Q96GB6; Q9NRF7; Q1-NOV-1997 (Rel. 435, Created) 28-FE2003 (Rel. 41, Last sequence update) 10-0CT-2003 (Rel. 42, Last annotation update) Membrane component, chromosome 17, surface marker 2 (Next to BRCA1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=21181710; PubMed=11285252;
MEDLINE=21181710; PubMed=11285252;
Nishimura D.Y., Searby C.C., Carmi R., Elbedour K., Van Maldergem I Fulton A.B., Lam B.L., Powell B.R., Swiderski R.E., Bugge K.E., Haider N.B., Kwitek-Black A.E., Ying L., Duhl D.M., Gorman S.M., Heon E., Iannaccone A., Bonneau D., Biesecker L.G., Jacobson S.G., Stone E.M., Sheffield V.C.,
Positional cloning of a novel gene on chromosome 16g causing Bardet-Blach syndrome (BBS2).";
Hum. Mol. Genet. 10:865-874(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .
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                                                                                                                                                                             65.4%; Score 34; DB 1; Length 551;
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                                                                                                     G -> A (IN REF. 2).
CECB2D70C8B1E0B6 CRC64;
                                                  COLLED COIL (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               28-FEB-2003 (Rel. 41, Created)
28-FBB-2003 (Rel. 41, Last sequence update)
20-CT-2003 (Rel. 42, Last annotation update)
Bardet-Biedl syndrome 2 protein homolog.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Brachydanio rerio (Zebrafish) (Danio rerio).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    715 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3; Mismatches
                                                                                                                                                                                                          61;
                                                                                                                                                                                                                               0; Mismatches
B BOX-TYPE 1.
B BOX-TYPE 2.
                                                                                                                                                                                                          Pred. No.
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InterPro; IPRO00413; Integrin_alpha.
Pfam; PF01839; FG-GAP; 2.
SEQUENCE 715 AA; 79125 MW.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; AF342739; AAK28555.1; -.
                                                                                                                               61591 MW;
                                                                                                                                                                                                       85.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4; Conservative
                                                                                                                                                                                                                                    6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
     132
182
249
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                                                                                                                                                                                                                                                                                                                                       361 SVPLYPC 367
     92
140
181
274
259
551 AA;
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Best Local Similarity
Matches 4; Conserv
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Hum. Mol
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ISOIA=Q14596-2; Sequence=VSP 004314;
Note=No experimental confirmation available;
-!- SIMILARITY: Contains 1 OPR domain.
-!- SIMILARITY: Contains 1 UBA domain.
-!- SIMILARITY: Contains 1 ZZ-type zinc finger.
-!- CAUTION: Was originally (Ref.1) thought to be the ovarian carcinoma antigen CA125.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Search completed: September
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          TISSUE-Lymph,

WELINE=22388257, PubMed=12477932,

Strausberg R.L., Peingold E.A., Grouse L.H., Derge J.G.,

Strausberg R.L., Peingold E.A., Grouse L.H., Derge J.G.,

Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Hopkins R.F., Jordan H., Moore T., Max S.I., Mang J., Hsieh F.,

Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Ronstein M.J., Uddin T.B., Toshiyuki S., Carninci P., Mullahy S.J.,

Browstein M.J., Uddin T.B., Toshiyuki S., Carninci P., Mullahy S.J.,

Raha S.S., Loquellano N.A., Perters G.J., Abramson R.D., Mullahy S.J.,

Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Nilalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Raha S.S., Colling A.C., Shevchenko Y., Bouffard G.G.,

Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

"Generation and initial analysis of more than 15,000 full-length

human and mouse colM sequences.",
                                                                                                                                                                                           TISSUE=Ovary;
MEDLINE=94348506; PubMed=8069304;
Campbell I.G., Nicolai H.M., Foulkes W.D., Senger G., Stamp G.W.,
Allan G., Boyer C., Jones K., Bast R.C. Jr., Solomon E., Trowsdale J.,
Black D.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=21100444; PubMed=11179671;
Dimitrov S., Brennerova M., Forejt J.;
Expression profiles and intergenic structure of head-to-head oriented Brcal and Nbrl genes ";
Gene 262:89-98 (2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=96051398; PubMed=7584044;
Nomura N., Nagase T., Miyajima N., Sazuka T., Tanaka A., Sato S., Seki N., Kawarabayasi Y., Ishikawa K.-I., Tabata S.;
"Prediction of the coding sequences of unidentified human genes. II. The coding sequences of 40 new genes (KTAA0041-KTAA0080) deduced by analysis of cDNA clones from human cell line KG-I.";
                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                       "A novel gene encoding a B-box protein within the BRCA1 region at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      [5]
SEQUENCE OF 412-508 FROM N.A.
MEDLINE=96090243; PubMed=7581362;
Harshman K., Bell R., Rosenthal J., Katcher H., Miki Y.,
Swenson J., Gholami Z., Frye C., Ding W., Dayananth P.,
Swenson J., Gholami Z., Frye C., Ding W., Thelpes R., Hatrier T.,
Stone S., Shaffer D., Bayer S., Hussey C., Tran T., Lai M.,
Rosteck P.R., Skolnick M.H., Shattuck-Eidens D., Kamb A.;
"Comparison of the positional cloning methods used to isolate the
                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A. (ISOFORM 1), AND VARIANT HIS-923.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
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gene 1 protein) (1A1-3B).
M17S2 OR NBR1 OR 1A13B OR KIAA0049.
Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  . Mol. Genet. 4:1259-1266(1995).
ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                                                                         Hum. Mol. Genet. 3:589-594(1994).
                                                                                                                                                                        SEQUENCE FROM N.A. (ISOFORM 1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A. (ISOFORM 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE OF 1-42 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DNA Res. 1:223-229(1994).
                                                                                                                       NCBI_TaxID=9606;
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PIISEDQTAALMARLFEMGFCDRQLNLRLLKKHNYNILQVV
PIELLQLNNNNDWYSQRY -> GLWGLLSFLHLAKKCFFLKAP
SEAFGWF (in isoform 2).
/FIId=VSP_004314.
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Pred. No. 1.1e+02;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      / FILE - ST. 1054385).
/FILE-VAR 016106.
LGDSMYSSALSQPGLERGAEGKPGV -> QAWSEVLKASLGF (IN REF. 1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             966 AA; 107432 MW; 6A057E7AA88BEAEF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR000270; OPR PB1.
InterPro; IPR000449; UBA_domain.
InterPro; IPR000449; UBA_domain.
InterPro; IPR000443; Znf_ZZ.
Pfam; PF00564; PB1; 1.
Pfam; PF00569; ZZi. 1.
SMART; SM000591; ZnF_ZZ; 1.
SMART; SM000591; ZnF_ZZ; 1.
PR0STTE; PS50030; UBA; 1.
PR0STTE; PS50130; Zr_ZZ_1; 1.
PR0STTE; PS501357; Zr_ZZ_2; 1.
Zinc_finger; Alternative splicing; Polymorphism.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ZZ-TYPE.
UBA.
                                                                                                                                                                                                          EMBL; X76952; CAA54274.1; -... EMBL; B30756; BAA66417.1; -... EMBL; BC009808; AAH09808.1; -... EMBL; AF27189; AAF74119.1; -... GMSL; AAA9328.1; -... GlycountedB; Q14596; -... GlycountedB; Q14596; -... Genew; HGNC:6746; M17S2.
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6; Conservative
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957
714
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Matches 6; Conserv
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IsoId=Q14596-1; Sequence=Displayed;

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		Description	11111111111111111111111111111111111111	Ogma88 arahidoneis	P91378 Caenorhahdi	Ogzive horrelia bu	OBUZIA DEL CITA DA COMPANION	Ogness virialla fac	030782 chlamidonhi	Obtmo dropping	OSEGE GROUPHILD	O22242 stabidonain	020243 arabinopara	O82777 PORC 221101V	Control and a spiral	Operation sapien	Opana musculu	OSS921 helicobacte	
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093368	07X9C0	096736	Q8BU71	QBR673	Q99Y31	Q8NZF5	Q87F37	Q8BN56	015716	Q8N787	Q8TVZ0	Q9M7A8	Q86KE8	Q9P7Q7	Q8NBV6	O9NOC0	086SP2	Q9BKR0	Q9BPY7	Q9BYT4	Q8Z306	Q8ZKM1	Q9PEG0	Q9BX88	OSTDUS	OPUEVS	081PZ5	Q01863	
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407	972	114	147	150	185	186	309	442	256	583	650	945	1348	1639	120	143	186	197	249	265	278	283	305	309	388	388	422	496	
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37	37	36	36	36	36	36	36	36	36	36	36	36	36	36	35	35	35	35		35						32		32	
17	18	19	20	21	22	23	24	25	26	27	28	53	30	31	32	33	34	35	36	3.7		39	40	41	42	43	44	45	

ALIGNMENTS

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¹ CISVPLVPC 9

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

¹⁰¹⁷⁰⁴¹ seqs, 315518202 residues Searched:

¹⁰¹⁷⁰⁴¹ Total number of hits satisfying chosen parameters:

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01-MXY-1999 (TrEMBLrel. 10, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Hypothetical protein.
Borrelia burgdorferi (Lyme disease spirochete).
Bacteria, Spirochaetes; Spirochaetales; Spirochaetales.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-007-2002 (TrEMBLrel. 22, Created)
01-007-2002 (TrEMBLrel. 22, Last sequence update)
01-007-2002 (TrEMBLrel. 22, Last annotation update)
Hypothetical protein FLJ25492.
Hypothetical protein FLJ25492.
Elwayotas (Hunan).
Elwayotas Metazoas (Chordata; Craniata; Vertebrata; Euteleostomi; Manalyia; Butheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                   DB 5; Length 362;
29;
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Pred. No. 10;
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                                                                                                                                                                                                                                                                                                                                                                    1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN=N40;
STRAIN=N40;
Feng S., Chen G., Barthold S.;
Feng S., Chen Borrelia burgdorferi.";
"G5 clone from Borrelia burgdorferi.";
Submitted (MAX-1997) to the EMBL/GenBank/DDBJ databases.
EMBL; AF005056; AAD01230.1; -.
Hypothetical protein.
Hypothetical protein.

80 AA; 9171 MW; C61A1E359DED8EA3 CRC64;
                                              "The sequence of C. elegans cosmid K12D9.";
Submitted (JAN-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                      to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                  Wilson R.; Submitted (JUN-2003) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                   F25CFD3B0E1D9435 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               134 AA.
                                                                                                                                                                                                                                                                                                                                   Score 39; DB 5; Pred. No. 29; 2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    80 AA
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                                                                                                                                                                                                                                                                                                     362 AA; 41292 MW;
                                                                                                                                                                                                                                                                                                                                       75.0%;
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Best Local Similarity 87.5%;
Matches 7; Conservative
                                                                                                                                                                                                                                                                    EMBL; U80030; AAG24161.2;
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                                                                                                                                                                                                                                                                                                                                                                          6; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                  233 CISLPIVTC 241
                                                                                                                                             Waterston R.;
Submitted (NOV-2002)
                                                                                                                                                                                                                                                                                                                                                                                                             1 CISVPLVPC 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       40 CISVPLYP 47
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TISSUE=Brain;
                                                                                                         SEQUENCE FROM N.A. STRAIN=Bristol N2;
                                                                                                                                                                                             SEQUENCE FROM N.A. STRAIN=Bristol N2;
SEQUENCE FROM N.A. STRAIN=Bristol N2;
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                                   Graves T.;
"The sequence of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=139;
                                                                                                                                                                                                                                                                                                       SEQUENCE
                                                                                                                                                                                                                                                                                                                                         Query Match
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Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                  Arabidopsis thaliana (Mouse-ear cress).
Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN=C. Columbia;
Lin X., Kaul S., Town C.D., Benito M., Creasy T.H., Haas B., Wu D.,
Ronning C.M., Koo H., Fujii C.Y., Utterback T.R., Barnstead M.E.,
Bowman C.L., Wite O., Nierman W.C., Fraser C.M.;
"Arabidopsis thaliana chromosome III BAC T12H1 genomic sequence.";
Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases.
EMBL, AC009177, AAF270371.; -.
GO; GO:0005509; F:calcium ion binding; IEA.
InterPro; IPR002048; EF-hand.
Pfam; PF000036; efhand; 2.
PROSITE; PS00018; EF HAND; 2.
SEQUENCE 648 AA; 73066 WW; D22FD23B724D8B7B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Genome sequence of the nematode C. elegans: a platform for investigating biology. The C. elegans Sequencing Consortium."; Science 282:2012-2018(1998).
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                                                                          Length 342;
                                                                                                             Indels
                                       342 AA; 37282 MW; 4651F38D116A8049 CRC64;
                                                                                                                                                                                                                                                                                        01-0CT-2000 (TrEMBLrel. 15, Created)
01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
T12H1.28 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ol-OCT-2003 (TrEMBLrel. 25, Last sequence update) 01-OCT-2003 (TrEMBLrel. 25, Last annotation update) Serpentine receptor, class w protein 121.
                                                                            78.8%; Score 41; DB 2; 77.8%; Pred. No. 11;
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                                                                                                               0; Mismatches
     PROSITE; PS00197; 2FE2S FERREDOXIN; 1.
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STRAIN=Bristol N2;
MEDLINE=99069613; PubMed=9851916;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              P91378;
01-MAY-1997 (TrEMBLrel. 03,
01-CT-2003 (TrEMBLrel. 25,
01-CCT-2003 (TrEMBLrel. 25,
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Matches 6, Conservative
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                                                                                              Best Local Similarity 77.8
Matches 7; Conservative
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                                                                                                                                                    1 CISVPLVPC 9
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SEQUENCE FROM N.A.
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                           Iron; Iron-sulfur
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=3702;
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Alvarenga R., Alves L.M.C., Arraya J.E., Baia G.S., Baptista C.S.,
Alvarenga R., Alves L.M.C., Arraya J.E., Baia G.S., Baptista C.S.,
A Alvarenga R.H., Bonaccorai E.D., Bordin S., Bove J.M., Briones M.R.S.,
Buenco M.R.P., Camarco A.A., Bordin S., Bove J.M., Briones M.R.S.,
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A Colauto N.B., Cristofani M., Dias-Neto E., Docena C., El-Dorry H.,
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A Fraga J.S., Mirama B.E., Caldman M.H.S., Gomes S.L., Gruber A.,
A Krieger J.E., Hoheisel J.D., Junqueira M.E., Kemper B.E., Kitajima J.P.,
A Krieger J.E., Miramae E.E., Laigret F., Lambais M.R., Leite L.C.C.,
A Machado M.A., Macleira A.M.B.N., Madeira H.M.F., Matsukuma A.Y.,
Marchado M.A., Macleira A.M.B.N., Machino C.L.,
Mandelra A.M.B.N., Martins E.M.F., Matsukuma A.Y.,
A Marchado M.A., Nascimento A.L.F.O., Netto L.E.S.,
Mhani A. M., Nobrega F.G., Nunes L.R., Oliveira M.A.,
A de Oliveira M.C., de Oliveira R.C., Palmieri D.A., Paris A.,
A de Silva A.C.R., da Silva A.M., da Silva F.R., Silva W.B., Jr.,
A da Silva A.C.R., da Silva A.M., Truffi D., Tsai S.M., Tsuhako M.H.,
A Sago M.A., Zatz M., Maidanis J., Setubal J.C.,
A Sago M.A., Zatz M., Weiloyski-Almeida S., Vettore A.L.,
A Sago M.A., Zatz M., Weiloyski-Almeida S., Vettore A.L.,
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Nishi T., Ota T., Nakagawa S., Senoh A., Mizuguchi H., Inagaki H., Suzuki Y., Hata H., Nakagawa K., Mizuno S., Morinaga M., Kawamura M. Sugiyama T., Irie R., Otsuki T., Sato H., Nishikawa T., Sugiyama A., Kawakami B., Nagai K., Isogai T., Sugano S.; "NEDO human cDNA sequencing project."; Submitted (JUL-2002) to the EMBL/GenBank/DDBJ databases.
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Nature 406:151-159(2000)
EMBL; AE003900; AAF83323.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;
Xanthomonadaceae; Xylella.
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                                                                                                                                                                                                                                                                                                                                                                                        4; Length 134;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2; Indels
                                                                                                                                                                                                                                                                Hypothetical protein.
SEQUENCE 134 AA; 13911 MW; 9605A9F9912C2802 CRC64;
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Last sequence update)
Last annotation update)
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Pred. No. 17;
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MEDLINE=20365717; PubMed=10910347;
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77.88;
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01-0CT-2000 (TrEMBLrel. 15,
01-JUN-2003 (TrEMBLrel. 24,
                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity 77.8 hes 7; Conservative
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SEQUENCE 154 AA;
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209 PFZ3
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Bannantine J.P., Rockey D.D., Hackstadt T.;
"Tandem genes of Chlamydia psittaci that encode proteins localized to
                                                Gaps
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Read T.D., Myers G.S.A., Brunham R.C., Nelson W.C., Paulsen I.T., Heidelberg J., Holtzapple E., Khouri H., Federova N.B., Carty H.A., Umayam L.A., Haft D.H., Peterson J., Beanan M.J., White O., Salzberg S.L., Hsia R.-C., McClarty G., Rank R.G., Bavoil P.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Genome sequence of Chlamydophila caviae (Chlamydia psittaci GPIC): examining the role of niche-specific genes in the evolution of the Chlamydiaceae.";
                                                                                                                                                                                                                                                                                                                                                                     Chlamydophila caviae.
Bacteria; Chlamydiae; Chlamydiales; Chlamydiaceae; Chlamydophila.
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Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Bhydroidea; Drosophilidae; Drosophila, NCBI_TaxID=7227;
      DB 16; Length 154;
19;
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                                                0; Indels
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                                                                                                                                                                                                                                                                01-JAN-1998 (TrEMBLrel. 05, Created)
01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-MAY-2000 (TrEMBLrel. 13, Created) 01-MAY-2000 (TrEMBLrel. 13, Last sequence update) 01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
                                                                                                                                                                                                                                198 AA.
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                                              2; Mismatches
        Score 38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Nucleic Acids Res. 31:2134-2147(2003).
EMBL; AF017105; AAC46378.1; -.
EMBL; AE016995; AAP05235.1; -.
                           Pred. No
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mol. Microbiol. 28:1017-1026(1998).
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                                                                                                                                                                                                                                                                                                                                 Inclusion membrane protein B.
      73.1%;
75.0%;
Query Match
Best Local Similarity 75.0
Matches 6; Conservative
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SEQUENCE 198 AA;
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Q9VN94
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MEDLINE=20083487; PubMed=10617197;
Lin X., Kaul S., Rounsley S.D., Shea T.P., Benito M.-I., Town C.D.,
Lin X., Kaul S., Rounsley S.D., Shea T.P., Benito M.-I., Town C.D.,
Fujii C.Y. Mason T.M., Bowman C.L., Barnstead M.E., Feldblyum T.V.,
Buell C.R., Ketchum K.A., Lee J.J., Ronning C.M., Koo H., Moffat K.S.,
Gronin L.A., Shen M., VanAken S.E., Umayam L., Tallon L.J., Gill J.E.,
Adams M.D., Carrera A.J., Creasy T.H., Goodman H.M., Somerrille C.R.,
Copenhaver G.P., Preuss D., Nierman W.C., White O., Eisen J.A.,
Salzberg S.L., Fraser C.M., Venter J.C.;
"Sequence and analysis of chromosome 2 of the plant Arabidopsis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
C. elegans Sequencing Consortium.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             73.1%; Score 38; DB 5; Length 568, 66.7%; Pred. No. 69;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Lin X.;
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                             STRAIN=Bristol N2;
Cordes M., Wohldmann P.;
"The sequence of C. elegans cosmid Y24D9A.";
Submitted (MAR-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                            Waterston R.;
Submitted (APR-2003) to the EMBL/GenBank/DDBJ databases
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GO; GO:0008026; F:ATP dependent helicase activity; IEA.
GO; GO:0016787; F:Hydrolase activity; IEA.
GO; GO:0003676; F:nucleic acid binding; IEA.
InterPro; IPR001410; DEAD.
InterPro; IPR001650; Helicase_C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    568 AA; 65908 MW; EE4299B1DCFBE98D CRC64;
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(TrEMBLrel. 11, Last sequence update)
(TrEMBLrel. 25, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Putative ATP-dependent RNA helicase A.
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  investigating biology. The C. Science 282:2012-2018(1998).
                                                                                                                                                                                                                                                                                                     EMBL; AC006729; AAX84599.2;
WormPep; Y24D9A.2; CE33849.
InterPro; IPR001214; SET.
Pfam; PF00856; SET; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ouery Match
Best Local Similarity 60...
                                                                                                                                                                                                                                                                                                                                                                                                   SMART; SM00317; SET; 1.
PROSITE; PS50280; SET; 1.
Hypothetical protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nature 402:761-768(1999)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 CISVPLVPC 9
                                                                                                                                                                                                              SEQUENCE FROM N.A. STRAIN=Bristol N2;
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                                                                        SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               022243;
01-JAN-1998
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                                                              Adams M.D. (Celliker S.E. ii P.W. Hoskins R.A., Gocayne J.D., RAMBDLIMES-1096006; FubMed=10718.1312;

Ramaratides P.G., Scherer S.E. ii P.W. Hoskins R.A., Galle R.P., George R.A., Lewis S.E., ii P.W. Hoskins R.A., Galle R.P., Scherer S.E., ii P.W. Hoskins R.A., Galle R.D., Sutton G.G., Wortman J.R., Yandell M.D., Zhang O., Chen L.X., Sutton G.G., Wortman J.R., Yandell M.D., Zhang O., Chen L.X., Sutton G.G., Wortman J.R., Yandell M.D., Zhang O., Chen L.X., Ramaratides G., Bardwin D., Belandon R.R., Mariol G.L. Bardwin D., Belandon C.R., Miklos G.L.G., Ballewin D., Bortchan M.R., Bouck J., Bayeaktaroglu L., Beasley E.M., Ballew R.M., Cawley S., Daller H., Cadteu E., Center A., Chandra I., Burtis R.C., Busan D.A., Buller H., Cadteu E., Center A., Chandra I., Burtis R.C., Busan D.A., Deng Z., Mays A.D., Dew I., Dietz S.M., Rockery S., Dallock P., Denger S., Dunkow B.C., Dunn P., Burtis R.C., Busan D.A., Bowler M., Dugan R.D., Dew I., Dew I., Dietz S.M., Re Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M., Re Pablos B., Delcher A., Howler S., Correll J.M., Gallock R., Goorge I. C., Ferriaz C., Ganar P., Harris M., Golg K., Gorrell J.H., Gallour P., Harris M., Harvey D., Hermandez J.R., Rednisson J.A., Revlate S., Rulp D., Lai Z., Alali M., Kalush F., Karaft C., Kravitz S., Kulp D., Lai Z., Alali M., Kalush F., Karaft C., Kravitz S., Kulp D., Lai Z., Liang Y., Liu X., Matted B., McIntosh T.C., McLeod M.P., McPherson D.L., Ram Hostin D. W., Nelson D.L., Ram Hostin D. W., Nelson D.L., Mouris J., Wollen D.R., Peller J., Wang K., Ban S., Pollard J., Puris S., Rulp D., Shen H., Spier E., Spradling A.C., Stapheton M., Stupsken D.S., Rang A.H., Wang Z., Shen S., Stone S., Shen S., Shen S., Shen S., Shen S., Stone S., Shen S., Stone S., Shen S., Stone S., Shen S., Shen S., Stone S., Shen S., Shen S., Shen S., Shen S., Shen S., Shen S., Shen S., Shen S., Shen S., Shen S., Shen S., Shen S., Shen S., Shen S., Shen S., Shen S., Shen S., Shen S., Shen S., Shen S., Shen S., Shen S., Shen S., Shen S., Shen S., Shen S.,
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Rhabditidae; Peloderinae; Caenorhabditis.
NCBI_TaxID=6239;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      73.1%; Score 38; DB 5; Length 562;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         562 AA; 63406 MW; AC09F5B6F5D2F970 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Last sequence update)
Last annotation update)
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2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-DEC-2001 (TrEMBLrel. 19, Created)
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MEDLINE=99069613; PubMed=9851916;
Wilson R.;
                                                    WEDLINE=20196006; PubMed=10731132;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-JUN-2003 (TrEMBLrel. 24, Loud-CCT-2003 (TrEMBLrel. 25, Loudypothetical protein Y24D9A.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              55.6%;
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Matches
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InterPro; IPR000571; Znf

RESULT 11 070244

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TISSUE—Thyroid;
Ninomiya K., Wagatsuma M., Kanda K., Kondo H., Yokoi T., Kodaira H.,
Puruya T., Takahashi M., Kikkawa E., Omura Y., Abe K., Kanihara K.,
Katsuta N., Sato K., Tanikawa M., Yamazaki M., Suzuki Y., Hata H.,
Nakagawa K., Mizuno S., Morinaga M., Kawamura M., Sugiyama T.,
Iris R., Otsuki T., Sato H., Nishikawa T., Sugiyama T.,
Nagai K., Isogai T., Sato H., Nishikawa T., Sugiyama A., Kawakami B.,
"NEDO human cDNA sequencing project.";
Submitted (UUL-2002) to the EMBL/GenBank/DDBJ databases.
BMBL; AK098419; BAC05303.1;
Hypothetical protein.
SEQUENCE 132 AA; 14716 MW; 8C266ICA0E87309B CRC64;
                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
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C TISSUE-Lung, Spleen, and Petal;
A Strausberg R.;
Submitted (DEC-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; BC041461, AAH41461.1; -.
EMBL; BC05507; Pscopper ion binding; IEA.
R O, GO:005507; Pscopper ion binding; IEA.
R InterPro; IPR007087; Znf C2H2.
R Pfam; PF00096; zf-CZH2; 5.
Probom; PD0000003; Znf CZH2; 5.
PROSITE; PS00080; WÜLTICOPPER_OXIDASE2; 1.
R PROSITE; PS00080; WÜLTICOPPER_OXIDASE2; 1.
R PROSITE; PS00088; ZINC_FINGER_CZH2_2; 5.
R PROSITE; PS0157; ZINC_FINGER_CZH2_2; 5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         71.2%; Score 37; DB 4; Length 132; 62.5%; Pred. No. 26; ative 3; Mismatches 0; Indels
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                                                                                                                                                 01-0CT-2002 (TrEMBLrel. 22, Created)
01-0CT-2002 (TrEMBLrel. 22, Last sequence update)
01-0CT-2002 (TrEMBLrel. 22, Last annotation update)
Hypothetical protein FLJ25553.
Homo sapiens (Human).
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01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Similar to snail homolog 3 (Drosophila) (Fragment).
                                                                                                       132 AA
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                                                                                                    PRT;
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Best Local Similarity 62.50,
Ther 5; Conservative
                                                                                                    PRELIMINARY;
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Best Local Similarity
Matches 6; Conserv
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SEQUENCE
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Q86SUS;
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                                               RESULT 12
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Masmussen H.H., Brault D., Pontillon F., Goda F.O., Christensen E.I.,
Hammond T.G., Verroust P.J.;
The intrinsic factor-vitamin Bl2 receptor and target of teratogenic
antibodies is a megalin-binding peripheral membrane protein with
thomology to developmental proteins.;
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Rattus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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                                                                                                                                                                                                                       73.1%; Score 38; DB 10; Length 1015; 75.0%; Pred. No. 1.2e+02; Live 1; Mismatches 1; Indels
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21 3623 INTRINSIC FACTOR-B12 RECEPTOR
3623 AA; 398981 MW; 39FB792AC6545240 CRC64;
Pfam; PR00271; helicase C; 1.
Pfam; PR0042; zf-CCCH; 2.
SMART; SM00497; DEXDC; 1.
SMART; SM00490; HELICC; 1.
SMART; SM0035; ZnF C3H1; 2.
ATP-binding; Helicase; Hydrolase.
SEQUENCE 1015 AA; 115084 MW; D1C342B338C561C9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-AUG-1998 (TrEMBLrel. 07, Created)
01-JAN-1999 (TrEMBLrel. 09, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT; 3623 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pfam; PF00431; CUB; 27.
Pfam; PF00008; EGF; 5.
SMART; SM001042; CUB; 26.
SMART; SM00179; EGF CA; 4.
PROSITE; PS00110; ASX HYPROXYL; 3.
PROSITE; PS01180; CUB; 27.
PROSITE; PS01180; EGF 2; 2.
PROSITE; PS01187; EGF 2; 2.
PROSITE; PS01187; EGF 2; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=98148073; PubMed=9478979;
                                                                                                                                                                                                                                                                              Conservative
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Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                   676 CVSVPFVP 683
                                                                                                                                                                                        Query Match
Best Local Similarity
'...a 6; Conserve
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Gaps

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313 CSQAPLVPC 321

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Search completed: September 5, 2004, 10:00:09
Mus musculus (Mouse)
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                                                                                                               Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
NCBI_TaxID=10090;
                                                               Q9QY31;
01-MAX-2000 (TrEMBLrel. 13, Last sequence update)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Snail-related zinc finger protein SWUC (Zinc finger protein 293).
SNAI3 OR ZFP293 OR SWUC.
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71.2%; Score 37; DB 11; Length 287;
Best Local Similarity 75.0%; Pred. No. 54;
Matches 6; Conservative 2; Mismatches 0; Indels
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                                                                                                                                                                   MEDLINE=20075155; PubMed=10606664;
                                                        PRT;
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Q8C244,
01-MAR-2003 (TrEMBLrel. 23, C1
01-MAR-2003 (TrEMBLrel. 23, La
01-OCT-2003 (TrEMBLrel. 25, La
Zinc finger protein 293.
                                                        PRELIMINARY;
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67 CISLPLLP 74
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58 CISLPLLP 65
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1 CISVPLVP
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STRAIN=B6;
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STRAIN=NOD;
MEDLINE-22554683; PubMed=12466851;
The FATOM Consortium,
the RIKEN Genome Exploration Research Group Phase I & II Team;
the RIKEN Genome Exploration Research Group Phase I will Team;
Analysis of the mouse transcriptome based on functional annotation of
60,770 full-length cDNAs.";
Nature 420:563-573(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                R MGD; MGI:1353563; Brais.

R MGD; MGI:1353563; Brais.

R GO; GO:0005667; C:transcription factor complex; IDA.

GO; GO:000300; F:transcription of transcription, DNA-dependent; IDA.

R GO; GO:0006355; P:tegulation of transcription, DNA-dependent; IDA.

InterPro; IPR000345; CvtC. heme.BS.

R InterPro; IPR000345; CvtC. heme.BS.

R InterPro; IPR000347; Znf. C2H2.

R Probm:

R PROSITE; PS000063; Znf. C2H2; 1.

R PROSITE; PS000063; Znf. C2H2; 1.

R PROSITE; PS000063; Znf. C2H2; 2; 1.

R PROSITE; PS000063; ZINC. FINGER. C2H2.1; 4.

R PROSITE; PS000063; ZINC. FINGER. C2H2.1; 4.

R PROSITE; PS000089; ZINC. FINGER. C2H2.2; 4.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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Local Similarity 75.0%; Pred. No. 54;
les 6; Conservative 2; Mismatches 0;
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                                                                                                                                         SEQUENCE FROM N.A.
                                                            NCBI_TaxID=10090;
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protein search, using sw model • OM protein

2004, 09:37:49; Search time 29.5455 Seconds (without alignments) 86.068 Million cell updates/sec Ď September Run on:

US-09-761-636A-14

CISVPLVPC 9 Perfect score: Sequence:

Gapop 10.0 , Gapext 0.5 **BLOSUM62** Scoring table:

1586107 segs, 282547505 residues Searched:

Total number of hits satisfying chosen parameters:

length: 0 length: 2000000000 sed Minimum DB Maximum DB

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

geneseqp2003as:* geneseqp2003bs:* Geneseq_29Jan04:* geneseqp1990s:* geneseqp2000s:* geneseqp2001s:* geneseqp2002s:* geneseqp1980s:* geneseqp2004s:* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Nocardia Nocardia VEGF base VEGF base N. gonorr Amino aci Human nuc Human pro VEGF base Human pro Drosophil Acinetoba Rat cubil Human sec Human 5' Aau04533 VEGF base Aau04532 VEGF base Human foe Novel hum VEGF base Chlamydia Zinc fing Description Aau04545 V Aau04542 V Abg20501 F Abg77742 N Abg77742 N Adb64366 I Abb57779 I Abb57779 I Abb57779 I Abd8366 I Abd8366 I Aau04526 1 Aar66216 1 Aay12860 Aao16348 Abu96694 Abp28862 8 Aaw85729 1 Adc38773 1 Ada55489 Aau04544 Aar81472 SUMMARIES AAR81472 AAU04545 AAU04542 AAM06501 ABG22400 ABP77742 AAY32174 AAY32174 ABB57779 ADB64366 AAY27020 AAG00458 AAY12860 AAO16348 ABU96694 ADA55489 AAU04532 AAU04526 AAR66216 ABP28862 AAW85729 ADC38773 AAU04533 DB Length 64 65 132 232 310 310 11 11 56 56 Query Match I 78.8 75.0 75.0 775 69.2 69.2 67.3 100.0 52 Result Š.

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ALIGNMENTS

Human; VEGF; vascular endothelial growth factor; angiogenesis; neovascularisation; lymphangiogenesis; psoriasis; tumour; diabetes induced neovascular sequelae; rheumatoid arthritis; diabetic retinopathy; chronic inflammation; cyclic. VEGF based monocyclic peptide 11. AAU04533 standard; peptide; 9 AA. (first entry 26-SEP-2001 AAU04533;

Location/Qualifiers
1. .9
/note= "This bond cyclises the peptide" Key Disulfide-bond Synthetic

WO200152875-A1.

26-JUL-2001

18-JAN-2001; 2001WO-US001533

18-JAN-2000; 2000US-0176293P. 16-MAY-2000; 2000US-0204590P.

(LUDW-) LUDWIG INST CANCER RES.

Stacker S, Achen MG, Hughes RA,

Cendron A;

WPI; 2001-442248/47

Novel monomeric monocyclic peptide, used to interfere with angiogenesis, or lymphanglogenesis, is produced by cyclizing a peptide loop fragment from an exposed loop of a growth factor protein by oxidizing the cysteine residues. Novel

Claim 49; Page 32; 102pp; English.

The sequence represents a monomeric monocyclic peptide of the invention, whose 3-dimensional structure is modelled on the expose loop of human VEGFD (vascular endothelial growth factor). The invention relates to a method of producing a monomeric monocyclic peptide by a measuring betabeta carbon separation distances on opposite antiparallel strands of a

Novel pro Human sec

Streptoco

residues.

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peptides toop integrate it is exposed in exposed in according cyclising the peptide by oxidising the cysteine residues. The monocyclic peptides, dimeric bicyclic peptides (comprising 2 linked monocyclic peptides) and a cyclic peptide with a teast one amino acid deleted prior concilisation are used to interfere with angiogenesis.

To cyclisation are used to interfere with angiogenesis.

The condition is diabetic retinopathy, psoriasing arthropathy, cerebrovascular secident, post-angioplasty restenosis, head, heat or cold trauma, substance-induced neovascularisation of the liver, excessive corresponded angiogenic dysfunction, diabetes induced neovascular sequelae, hypertension induced neovascular sequelae, nypertension induced neovascular sequelae, hypertension induced neovascular sequelae, or chronic liver sequelae, hypertension induced neovascular sequelae, or chronic liver accumulation in peripheral limbs or in lungs, peritoneal cavity, pleura, cor brain. The peptides are used to image blood vessels and lymphatic cor brain. The peptides are used to image blood vessels and lymphatic cor brain the neoripheral limbs or in lungs, peritoneal cavity, pleura, cor brain the least one biological activity induced by VEGF. VEGF-C or -D and care also used in combination with an anti-inflammatory agent, to treat a correction in peritone with an anti-inflammatory agent, to treat a chronic inflammation, especially rheumatoid arthritis, psoriasis and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Novel monomeric monocyclic peptide, used to interfere with angiogenesis, or lymphangiogenesis, is produced by cyclizing a peptide loop fragment from an exposed loop of a growth factor protein by oxidizing the cysteine
peptide loop fragment from an exposed loop of a growth factor protein and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human; VEGF; vascular endothelial growth factor; angiogenesis; neovascularisation; lymphangiogenesis; psoriasis; tumour; diabetes induced neovascular sequelae; rheumatoid arthritis; diabetic retinopathy; chronic inflammation; cyclic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Indels

    10 .10 /note= "This bond cyclises the peptide"

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100.0%; Pred. No. 1.4e+06;
ive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 9 AA;
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The sequence represents a monomeric monocyclic peptide of the invention, whose 3-dimensional structure is modelled on the expose loop of human whose 3-dimensional structure is modelled on the expose loop of human construction relates to a method of producing a monomeric monocyclic peptide by a measuring beta carbon separation distances on opposite antiparallel strands of a peptide loop fragment from an exposed loop of a growth factor protein and cyclic peptides (comprising 2 linked monocyclic peptides) and a cyclic peptide with at least one amino acid deleted prior corpitation are used to interfere with angiogenesis.

CC cyclisation are used to interfere with angiogenesis.

CC corpitation are used to interfere with angiogenesis.

CC characterised by angiogenesis, neovascularisation or lymphangiogenesis.

CC characterised by angiogenesis, neovascularisation of the liver, excessive creamns substance-induced neovascularisation of the liver, excessive creamns unduced neovascular sequelae, hypertension induced neovascular sequelae, neovascular confiction. The peptides are also used to modulate vascular permeability in a mammal (the mammal has a condition diabetes induced neovascular confiction in peripheral limbs or in lungs, peritoneal capity, pleura, or brain. The peptides are used to indeption or brain. The peptides are also used to indeption are used to interfere with at least one biological activity induced by VEGF, VEGF-C or -D and characterise are also used in combination with an unit infilammatory agent, to treat a characterise are also used in combination with an anti-inflammatory of the treat and previous peritonic inflammation in peripherally with an anti-inflammatory of are also and archiris inflammation in peripherally. The mannally archirate and province in the mannal activity i
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Pred. No. 2.2;
0; Mismatches 0; Indels

    11 .11 /note= "This bond cyclises the peptide"

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                                     Claim 49; Page 32; 102pp; English.
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16-MAY-2000; 2000US-0204590P.
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Best Local Similarity 90.v
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93JP-00105171

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Cendron A;
                             Claim 49; Page 32; 102pp; English.
      Stacker S,
(LUDW-) LUDWIG INST CANCER RES.
     Hughes RA,
          WPI; 2001-442248/47.
     Achen MG,
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Score 41; DB 4 Pred. No. 2.9; 0; Mismatches 78.8%; 81.8%; 9; Conservative 11 σ |||||||| CISVPLTSVPC 1 CISVPL--VPC Local Similarity Sequence 11 AA; Query Match Matches ò

1;

Gaps 2.

4; Length 11; 0; Indels

> 16-OCT-2003 04-AUG-1995 AAR66216;

alkene monoxygenase; reductase; epoxidation; amoD. Nocardia corallina reductase (encoded by amoD). AAR66216 standard; protein; 342 AA. (first entry) (revised)

93JP-00105171 06-APR-1993; 21-0CT-1994

Gordonia rubripertinctus.

JP06292571-A

Alkene mon:oxygenase and corresp. gene - useful for the epoxidation of an E.coli transformed with the DNA sequence AAQ79569 are able to catalyse the epoxidation of alkenes. The DNA is derived from Nocardia corallina and comprises 4 open reading frames. ORFs amoA and amoC encode subunits and 2 of the alkene monoxygenase enzyme and ORF amoD encodes a reductase capable of transferring electrons from NADH coenzyme to a monoxygenase. (Updated on 16-OCT-2003 to standardise OS field) AAR81472 standard; protein; 342 AA. Claim 2; Page 4-5; 30pp; Japanese. Query Match Best Local Similarity 77.8%; (NIHA) JAPAN ENERGY CORP WPI; 1995-009069/02 CISVPLVPC CASVPLEPC N-PSDB; AAQ79569 Sequence 342 AA; 06-APR-1993; 16-OCT-2003 07-AUG-1996 Н AAR81472; alkene. RESULT 5 AAR81472 à 엄 The sequence represents a monomeric monocyclic peptide of the invention, whose 3-dimensional structure is modelled on the expose loop of human values and of vascular endothelial growth factor). The invention relates to a method of producing a monomeric monocyclic peptide by a measuring betabet a carbon separation distances on opposite antiparallel strands of a cyclising the peptide by oxidising the cystein ersidues. The monocyclic peptides, dimeric bicyclic peptides (comprising 2 linked monocyclic peptides) and a cyclic peptide with at least one amino acid delated prior or cyclisation are used to interfere with angiogenesis.

Co cyclisation are used to interfere with angiogenesis, neovascularisation or lymphangiogenesis in a mammal with a condition. The condition is diabetic retinopathy, psoriasis arthropathy, hemangioma, vascularised malignant or benign tumour, post-recovery cerebrovascular accident, post-angioplasty restenosis, head, heat or cold trauma, substance-induced neovascularisation of the liver, excessive conference-induced neovascular sequelae, or chronic liver in fertion. The peptides are also used to modulate vascular permeability accumulation in peripheral limbs or in lungs, peritoneal cavity, pleura, or brain. The peptides are also used to inage blood vessels and lymphatic vasculature. The monomeric and bicyclic peptides are also used to interfere with at least one biological activity induced by VEGF. Core or and are also used to condition are also used to circuic and activity induced by vasculature to treat a chonic inflammation, especially rheumatoid arthritis, psoriasis and circuic renimants. Novel monomeric monocyclic peptide, used to interfere with angiogenesis, or lymphangiogenesis, is produced by cyclizing a peptide loop fragment from an exposed loop of a growth factor protein by oxidizing the cysteine

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Gaps 0;

Length 342; 2; Indels

Score 41; DB 2; Pred. No. 86; Mismatches

78.8%;

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83

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Alkene mono-oxygenase; indole; indigo production; biosynthesis; Nocardia corallina alkene mono-oxygenase gene product, amoD. Gordonia rubripertinctus; B-276. (first entry) microbial oxidation; dye. (revised)

94JP-00179688 94JP-00179688 38-JUL-1994; JP08023988-A. 08-JUL-1994; 30-JAN-1996

(NIHA) JAPAN ENERGY CORP. WPI; 1996-133426/14. N-PSDB; AAT17418. Prepn. of indigo by a microbiological method - by culturing a microbe having alkene monoxigenase activity to oxidise indole to indigo. Claim 5; Page 8-9; 11pp; Japanese. AAR81469-R81472 are protein products of the Nocardia corallina strain B-276 alkene mono-oxygenase gene. The gene encodes 4 protein products amoh, amob, amob, amob darived from the 3 different reading frames of the operon. The gene is useful for the production of indigo via oxidation of indole. Nocardia corallina can be cultured in a medium cong. indole and will readily oxidise the indole yielding indigo into the culture medium. E. coli may also be transformed with the alkene mono-oxygenase gene and (Updated on 16-OCT-2003 to standardise OS field)

à g

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Matches
                                                                                                                                                                                                                                                          RESULT 7
                                                                                                                                                                                                                                                                       AAU04542
                                                                                                                                                             Best
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The sequence represents a monomeric monocyclic peptide of the invention, whose 3-dimensional structure is modelled on the expose loop of human converse to a relate to a method of producing a monomeric monocyclic peptide by a measuring beta method of producing a monomeric monocyclic peptide by a measuring beta carbon separation distances on opposite antiparallel strands of a peptide loop fragment from an exposed loop of a growth factor protein and cyclising the peptides, dimeric bicyclic peptides (comprising 2 linked monocyclic peptides, dimeric bicyclic peptides (comprising 2 linked monocyclic peptides) and a cyclic peptide with at least one amino acid deleted prior cyclisation are used to interfere with angiogenesis.

To cyclisation are used to interfere with angiogenesis.

The condition is diabetic retinopathy, psoriasis, ruthropathy, condition is diabetic retinopathy, psoriasis, arthropathy, condition is diabetic retinopathy, psoriasis, arthropathy, concerebrowscular accident, post-angioplasty restences; head, heat or cold cramma, substance-induced neovascularisation of the liver, excessive concerebrace, hypertension induced neovascular sequelae, or chronic liver or chronic liver.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Novel monomeric monocyclic peptide, used to interfere with angiogenesis, or lymphangiogenesis, is produced by cyclizing a peptide loop fragment from an exposed loop of a growth factor protein by oxidizing the cysteine
                                                                Gaps
                                                                ö
                                                                                                                                                                                                                                                                       Human; VEGF; vascular endothelial growth factor; anglogenesis;
                                                                                                                                                                                                                                                                                 neovascularisation; lymphangiogenesis; psoriasis; tumour; diabetes induced neovascular sequelae; rheumatoid arthritis; diabetic retinopathy; chronic inflammation; cyclic.
                                       Length 342;
                                                                2; Indels
                                                                                                                                                                                                                                                                                                                                                                                     /note= "This bond cyclises the peptide"
                                       DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Cendron A;
                                                    86;
                                                                Mismatches
                                                    Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Example 25; Page 47; 102pp; English.
                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Stacker S,
                                                                                                                                                                           AAU04545 standard; peptide; 11 AA
                                                                                                                                                                                                                                                 monocyclic peptide 23.
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0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   18-JAN-2000; 2000US-0176293P.
16-MAY-2000; 2000US-0204590P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             18-JAN-2001; 2001WO-US001533.
                                       78.8%;
77.8%;
                                                                                                                                                                                                                            26-SEP-2001 (first entry)
                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hughes RA,
                                                                                                              CASVPLEPC 83
                                                                                        CISVPLVPC 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2001-442248/47.
                                       Query Match
Best Local Similarity
Matches 7; Conserv
                 Sequence 342 AA;
                                                                                                                                                                                                                                                                                                                                                                          Disulfide-bond
                                                                                                                                                                                                                                                                                                                                                                                                              WO200152875-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                      26-JUL-2001
                                                                                                                                                                                                                                                   VEGF based
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Achen MG,
                                                                                                                                                                                                                                                                                                                                       Synthetic
                                                                                                                                                                                                     AAU04545;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   residues.
                                                                                         Н
                                                                                                                75
                                                                                                                                                       RESULT 6
                                                                                                                                                                  AAU04545
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The sequence represents a monomeric monocyclic peptide of the invention, whose 3-dimensional structure is modelled on the expose loop of human vEGPD (vascular endothellal growth factor). The invention relates to a method of producing a monomeric monocyclic peptide by a measuring beta carbon separation distances on opposite antiparallel strands of a peptide loop fragment from an exposed loop of a growth factor protein and cyclising the peptide by oxidising the cysteine residues. The monocyclic peptides, dimeric bicyclic peptides (comprising 2 linked monocyclic peptides) and a cyclic peptide with at least one amino acid deleted prior
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infection. The peptides are also used to modulate vascular permeability in a mammal (the mammal has a condition characterised by fluid accumulation in peripheral limbs or in lungs, peritoneal cavity, pleura, or brain. The peptides are used to image blood vessels and lymphatic vasculature. The monomeric and bicyclic peptides are used to interfere with at least one biological activity induced by VBGF. Or -D and are also used in combination with an anti-inflammatory agent, to treat a chronic inflammation, especially rheumatoid arthritis, psoriasis and diabetic retinopathy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human; VEGF; vascular endothelial growth factor; angiogenesis; neovascularisation; lymphangiogenesis; psoriasis; tumour; diabetes induced neovascular sequelae; rheumatoid arthritis; diabetic retinopathy; chronic inflammation; cyclic.
                                                                                                                                                                                                                                                                                                                                                                                                                   Score 40; DB 4; Length 11;
Pred. No. 4.2;
1; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAU04542 standard; peptide; 11 AA
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16-MAY-2000; 2000US-0204590P.
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                                                                                                                                                                                                                                                                                                                                                                                                                             76.9%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity 72.7
8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         |:|||| ||| CVSVPLTTVPC 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 CISVPL--VPC 9
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                                                                                                                                                                                                                                                                                                                                                              Sequence 11 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Synthetic
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                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
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Characterised by angiogenesis, neovascularisation or lymphangiogenesis.

Characterised by angiogenesis, neovascularisation or lymphangiogenesis.

Che condition is diabetic retinopathy, psoriasis, arthropathy.

Che condition is diabetic retinopathy, psoriasis, arthropathy.

Cerebrovascular accident, post-angioplasty restenosis, head, heat or claume, substance-induced neovascularisation of the liver, excessive craume, substance-induced neovascular sequelae, or chronic liver infection. The peptides are also used to modulate vascular permeability in a mammal (the mammal has a condition characterised by fluid accumulation in peripheral limbs or in lungs, peritoneal cavity, pleura, or brain. The peptides are used to image blood vessels and lymphatic vasculature. The monomeric and bicyclic peptides are used to interfere with at least one bhological activity induced by VEGF, VEGF-C or -D and chronic inflammation, especially rheumatoid arthritis, psoriasis and althritis, psoriasis and althritis, psoriasis and althritis.
cyclisation are used to interfere with angiogenesis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     diabetic retinopathy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 11 AA;
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Gaps
                            5
 Score 39; DB 4; Length 11;
Pred. No. 6.2;
1; Mismatches 0; Indels
  75.0%;
                         Conservative
                                             1 CISVPL--VPC 9
          Local Similarity
nes 8; Conserv
Query Match
                      Matches
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11 CLSVPLTSVPC

g

RESULT

Human foetal protein, SEQ ID NO: 232. AAM06501 standard; protein; 101 AA. (first entry) 05-OCT-2001 AAM06501;

Human; foetal protein; cytostatic; immunosuppressive; immunostimulant; nootropic; neuroprotective; thrombolytic; osteopathic; antiinflammatory; gene therapy; antisense therapy; cancer; immune disorder; growth disorder; osteoporosis; thrombolytic disorder; nervous system disorder; inflammation.

Homo sapiens

WO200155339-A2

02-AUG-2001

25-JAN-2001; 2001WO-US002723

2000US-00491404 2000US-00663870 25-JAN-2000; 2000US-00491404 15-SEP-2000; 2000US-00663870 06-NOV-2000; 2000US-00707351

HYSEQ INC. HASE-)

Tang YT; Drmanac RA, Boyle BJ, Arterburn MC, Zhou P, Werhman T; WPI; 2001-465571/50. Ford JE, Asundi V, N-PSDB; AAH94176, Yeung G, Liu C, A

Claim 10; Page 264; 715pp; English

Novel fetal proteins useful for the treatment and diagnosis of diseases associated with dysfunction of the protein e.g. cancers, immune disorders, growth disorders, thrombolytic disorders, nervous system disorders and inflammation.

polypeptide and polynucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity

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0;
The invention relates to novel foetal polypeptides encoded by polymuclectides comprising one of 477 sequences fully defined in the specification. The foetal polymuclectides and polypeptides are useful in the treatment and diagnosis of diseases such as cancers, immune disorders, growth disorders (e.g. osteoporosis), thrombolytic disorders, nervous system disorders and inflammation. The present sequence is a polypeptide encoded by a cDNA assembled using an expressed sequence tag (EST) found to be expressed in human foetal tissue cDNA libraries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention relates to isolated polymucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polymucleotides are also used genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II) and (II) are useful for treating disorders involving a food sites expressing (II). (II) and (II) are useful for treating disorders involving a berrant protein expression or biological activity. The
                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder.
                                                                                                                                                                                                                                    .
                                                                                                                                                                                               Score 39; DB 4; Length 101;
Pred. No. 55;
                                                                                                                                                                                                                                    1; Indels
                                                                                                                                                                                                                                Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 20; SEQ ID NO 52759; 103pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Novel human diagnostic protein #22391.
                                                                                                                                                                                                                                                                                                                                                                                      ABG22400 standard; protein; 102 AA.
                                                                                                                                                                                              75.0%;
87.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    30-MAR-2001; 2001WO-US008631.
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2000US-00649167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Tang YT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                  Conservative
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Best Local Similarity
7; Conserv?
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                                                                                                                                                                                                                                                               1 CISVPLVP
                                                                                                                                                                                                                                                                                                 2 CISVPLTP
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                                                                                                                                                           Sequence 101 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       31-MAR-2000;
23-AUG-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     biodiversity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                    RESULT 9
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AAY27025 standard; protein; 44 AA.
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and to produce other types of data and products dependent on DNA and amino acid sequences. ABG00010-ABG30377 represent novel human diagnostic amino acid sequences of the invention. Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO at the wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present invention relates to proteins from Neisseria gonorrhoeae. Also disclosed are the nucleic acid molecules encoding the proteins and antibodiss that specifically bind to the proteins. The composition comprising the protein, nucleic acid or antibody is useful for the manufacture of a medicament for treating or preventing N. gonorrhoeae infection, this may be in the form of a vaccine or gene therapy. Sequences given in records ABPP6736-ABP81046 represent nucleic acid molecules of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              manufacture of
                                                                                                                                                                   Gaps
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medicament for treating or preventing N. gonorrheae infection.
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Pred. No. 1.9e+02;
2; Mismatches 0; Indels
                                                                                                                                     DB 4; Length 102;
                                                                                                                                                                   1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                            Antibacterial; infection; vaccine; gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                              N. gonorrhoeae amino acid sequence SEQ ID 2014.
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                                                                                                                                                   Pred. No. 56;
                                                                                                                                      Score 39;
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                                                                                                                                                                                                                                                                                                      ABP77742 standard; protein; 347 AA.
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                                                                                                                                      75.0%;
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                                                                                                                                                                    Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          Neisseria gonorrhoeae
                                                                                                                                                                                                                     24 CFSVPLVP 31
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                                                                                                                                                                                                  1 CISVPLVP 8
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                                                                                                                                     Query Match
Best Local Similarity
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                                                                                                            Sequence 102 AA;
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                                                                                                                                                                    Matches
                                                                                                                                                                                                                                                                            RESULT 10
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셤 ਨੇ

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The invention relates to a rat cubilin protein. Cubilin is a ligand-
binding, epithelial glycoprotein receptor that facilitates uptake of
intrinsic factor/vitamin Bl2 complexes in intestines and Kidney. It is
also involved in endocytosis and trafficking of light immunoglobulin
claims in renal proximal tubule cells. Host cells containing a vector
comprising the rat cubilin DNA sequence can be used for the recombinant
expression of the protein. Cubilin, or its fragments, are used to treat
or reduce toxicity, particularly in Kidneys, spheen, brain, liver, heart
and thyroid. Cubulin mutations may also be implicated in idiopathic
proteinuria, fetal malformation, poor fetal development and spontaneous
proteinuria, fetal malformation, poor fetal development and spontaneous
proteinuria, fetal malformation, poor fetal development and spontaneous
corrections. Cubilin may also be used to raise specific antibodies, used
for its detection, or clones that express it, in standard immunoassays.
Fragments of cubilin DNA can also be used to detect cubulin mRNA in cell
and tissues, by hybridization. Abnormal levels of cubilin in the urine
are indicative of kidney damage. Sequences ANI27021-35 represent EGF
repeat sequences of rat cubilin and from homologous regions of other
                                                                                                                                                                   Cubilin, epithelial glycoprotein receptor; vitamin B12; endocytosis; toxicity; kidney; spleen; brain; liver; heart; thyroid; abortion; rat; proteinuria; fetal malformation; fetal development; kidney damage; EGF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New DNA encoding cubilin, used for treating toxicity, particularly nephrotoxicity, and as marker of kidney damage.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
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ص
                                                                                                                  Amino acid sequence of rat cubilin EGF5 repeat.
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Pred. No. 35;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (TULA ) TULANE EDUCATIONAL FUND.
(INRM ) INST NAT SANTE & RECH MEDICALE.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Example 18; Fig 6A; 135pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             73.1%;
66.7%;
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(first entry)
                                                                (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Verroust PJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       12 CSQAPLVPC 20
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                W09937757-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  21-JAN-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          22-JAN-1998;
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01-FEB-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hammond TG,
                                                                08-OCT-1999
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                                                                                                                                                                                                                                                                                                           Rattus sp.
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AAY27025;
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Gaps

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Local Similarity 75.0 nes 6; Conservative

Best Loc Matches

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RESULT 11

CISVPLVP 8

--1 156 Otsuki T, Wakamatsu A, Sato H, Ishii S; Hio Y, Otsuka K, Nagai K, Irie R, Tamechika I; Otsuka M, Nagahari K, Masuho Y;

(HELI-) HELIX RES INST. (REAS-) RES ASSOC BIOTECHNOLOGY.

Isogai T, Sugiyama T, Yamamoto J, Isono Y, Seki N, Yoshikawa T,

WPI; 2003-450961/43. N-PSDB; ADB62396.

28-MAR-2002; 2002EP-00007401 05-NOV-2001; 2001JP-00379298 25-JAN-2002; 2002US-00350978 polynucleotides and polypeptides, useful for developing a diagnostic ker or medicines for regulation of their expression and activity, or

Claim 1; Page; 222pp; English.

as targets of gene therapy

marker

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The invention discloses a polynuclectide comprising a sequence selected from 1970 fully defined nucleotide sequences which encode novel colypeptides. Also claimed is a polypeptide encoded by the polynuclectide or its partial peptide, an antibody binding to the polypeptide or peptide or peptide of the polynuclectide by contacting the polypeptide or peptide or peptide by contacting the polypeptide or peptide or peptide by contacting the polypeptide or peptide or the polynuclectide by contacting the polypeptide or peptide or peptide between the two, a transformant carrying the polynuclectide in an expressible manner and an antisense polynuclectide. The oligonuclectide is useful as a primer for synthesising the polynuclectide and encoded or suseful as paramaceutical agents and many disease-related or genes may be included in them, for developing a diagnostic marker or medicines for regulation of their expression and activity, or as targets or genes therapy. The genes are involved in tissue and/or cell creamscription-related proteins, signal transduction-related proteins, creameration. Membrane proteins, signal transduction-related proteins, creameration to transcription-related proteins, diseases (e.g. osteoporosis, the activity or expression of the encoded protein to treat diseases. The concurry or expression of the encoded protein to treat diseases. The sequence data for this patent is not represented in the printed concerns between the printed in the printed or sequence or sequence data for this patent is not represented in the printed or sequence or sequence or sequence or sequence or sequence or sequence or sequence or sequence or sequence or sequence or sequence or sequence or sequence or sequence or sequence or sequence or sequence or sequence or sequence or sequence or sequence or sequence or sequence or sequence or sequence or sequence or sequence or sequence or sequence or sequence or sequence or sequence or sequence or sequence or sequence or sequence or sequence or sequence or sequence or sequence or se
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This sequence represents novel infection-specific protein IncB of chlamydia psittaci strain GPIC. IncB is found in the inclusion membrane of infected cells. It is associated primarily with the vegetative reticulate body form of Chlamydia rather than with the refractile elementary body form. The invention includes: a vaccine directed against the reticulate body form of Chlamydia comprising 1 or more infection-specific proteins (see AAY3170-78), including IncA, IncB and IncC; methods of using and producing such a vaccine; methods for detection of mifection-specific antibodies or antigens in a biological specimen; and a method of using therapeutic agents specifically directed against infection-specific peptides, or the genes that code for such peptides, to reat, chlamydial infection. (Updated on 17-OCT-2003 to standardise OS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Novel bacterial infection specific proteins for treating and diagnosing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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Chlamydia psittaci infection-specific protein IncB.
                                                            IncB; infection; vaccine; therapy; diagnosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 1; Page 41-42; 56pp; English.
                                                                                                                                                                                                                                                                                                                                                98US-0082438P.
98US-0082588P.
98US-0086450P.
                                                                                                                                                                                                                                                                                                99WO-US008744
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Rockey DD, Bannantine JP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (UYOR-) UNIV OREGON STATE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         157 CISLPIISC 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       chlamydial infections
                                                                                                                     Chlamydophila caviae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 CISVPLVPC 9
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 198 AA;
                                                                                                                                                                           WO9953948-A1
                                                                                                                                                                                                                                                                                                                                                                              21-APR-1998;
22-MAY-1998;
                                                                                                                                                                                                                                                                                                20-APR-1999;
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                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                Drosophila; developmental biology; cell signalling; insecticide;
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0
                            Score 38; DB 7; Length 208;
Pred. No. 1.6e+02;
1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                    Drosophila melanogaster polypeptide SEQ ID NO 129.
                                                              1; Mismatches
                                                                                                                                                                                                      ABB57779 standard; protein; 562 AA.
                            73.1%;
                                                                                                                                                                                                                                                                     26-MAR-2002 (first entry)
                                                              6; Conservative
                                                                                                                        33 CASLPLSPC 41
                                                                                            1 CISVPLVPC 9
                            Query Match
Best Local Similarity
Matches 6; Conserv
Sequence 208 AA;
                                                                                                                                                                                                                                                                                                                                                    pharmaceutical
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Drosophila melanogaster.
ABB57779
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AC ABB5
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AC ABB5
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DT 26-h
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KW Drost
KW Drost
KW Drost
XX
COST
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Human, pharmaceutical, diagnostic, gene therapy, tissue regeneration; cell regeneration, membrane protein, signal transduction-related protein, transcription-related protein, osteoporosis, neurological disease,

cancer; tumour

EP1308459-A2

07-MAY-2003

Homo sapiens

Human protein encoded by clone FCBBF30171230.

ADB64366

ID ADB64366

XX

AC ADB64

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DT 04-DE

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Human

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Cance

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(first entry)

04-DEC-2003

ADB64366;

ADB64366 standard; protein; 208 AA.

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Acinetobacter baumannii; bacterial disease; antibacterial; vaccine;
                                                                                                                                                                                                                        Acinetobacter baumannii protein #2775.
                                                                                                                                                                                                                                                                                       (GENO-) GENOME THERAPEUTICS CORP.
                                                                                                                                                                                                                                             Acinetobacter baumannii
                                                                                                                                                                                                                                     plant biocontrol agent
                                                                                                                                                                                                                                                                                                       WPI; 2003-576092/54
                                                                                                                                                                                                                                                                                                            N-PSDB; ADA31488
                                                                                                                                                                                                                                                      US6562958-B1
                                                                                                                                                                                                                                                                       04-JUN-1999;
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                                                                                                                                                                                                                20-NOV-2003
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                                                                                                                                                                                                                                                                                               Breton G,
                                                                                                                                                 Query Match
                                                                                                                                                                                       RESULT 15
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98US-0088701P. 99US-00328352

Bush D;

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New Acinetobacter baumanni proteins and nucleic acids, useful as reagents for diagnosing a bacterial disease, as components of antibacterial vaccines, as targets for antibacterial drugs, or as biocontrol agents for
                                                                                                                                                                         The invention relates to isolated Acinetobacter baumannii nucleic acids. The A. baumannii nucleic acids and polypeptides are useful as reagents for diagnosing a bacterial disease, as components of antibacterial vaccines, as targets for antibacterial drugs, to detect the presence of A. baumannii and other Acinetobacter species in a sample, in screening compounds for the ability to interfere with the A. baumannii life cycle or to inhibit A. baumannii infection, and as biocontrol agents for plants. The present sequence represents the amino acid sequence of an A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 38; DB 6; Length 589;
Pred. No. 4.6e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Search completed: September 5, 2004, 09:55:23 Job time : 31.5455 secs
                                                                                                                                      Example; SEQ ID NO 6901; 328pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               73.1%;
77.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           273 CISVPLFHC 281
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                                                                                                                                                                                                                                                                                                                                                                                  baumannii protein
                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 589 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention is useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL16175) and the encoded proteins (ABBS7137-ABB72072). The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from MIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                    New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signaling and cell-cell interactions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure; SEQ ID NO 129; 21pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 38; DB 4; Length 562; Pred. No. 4.4e+02; 2; Mismatches 2; Indels
                                                                                                                                                                                                                                                                     Li PWD, Myers EW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          73.1%;
55.6%;
                                                                                                23-MAR-2001; 2001WO-US009231.
                                                                                                                                           23-MAR-2000; 2000US-0191637P.
11-JUL-2000; 2000US-00614150.
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Matches 5; Conservative
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                                                                                                                                                                                                                                                                       Adams M,
                                                                                                                                                                                                                                                                                                                       WPI; 2001-656860/75.
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WO200171042-A2
                                                                                                                                                                                                                                                                     Venter JC,
                                                  27-SEP-2001
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Gaps

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2; Indels

us-09-761-636a-14.open.rapb

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RESULT 2
US-09-761-636A-13
Sequence 13, Application US/09761636A
; Parent No. US20020065218A1
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Sequence 13, Appl
Sequence 26, Appli
Sequence 21, Appli
Sequence 21, Appl
Sequence 219, Appl
Sequence 219, Appl
Sequence 18427,
Sequence 18427,
Sequence 18427,
Sequence 25, Appl
Sequence 25, Appl
Sequence 25, Appl
                                                                                                5; Search time 25.2727 Seconds (without alignments) 112.199 Million cell updates/sec
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" cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*

" cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*

" cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep:*

" cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep:*

" cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep:*

" cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*

enCore version 5.1.6
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US-09-761-636A-13
US-09-761-636A-7
US-09-761-636A-2
US-09-761-636A-23
US-09-761-636A-23
US-10-1437-963-181998
US-10-10-404-2520
US-10-087-192-519
US-10-424-599-158427
US-10-424-599-158427
US-10-94-749-3057
US-10-437-963-148570
US-10-424-599-168425
US-10-437-963-148570
US-10-424-599-168425
                                                                                                                                                                                                                                                                                                                     Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                          1298764 seqs, 315065143 residues
                                                                                                  September 5, 2004, 10:00:15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Published Applications AA *
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Maximum Match 100%
Listing first 45 summaries
                                                                OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                           Minimum DB seq length: 0
Maximum DB seq length: 200000000
                                                                                                                                                                      US-09-761-636A-14
52
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Match Length DB
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Perfect score:
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Sequence 131, App
Sequence 225406,
Sequence 162402,
Sequence 162997,
Sequence 267602,
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Sequence 44103, A
Sequence 43762, A
Sequence 9, Appli
Sequence 110, App
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Sequence 1
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APPLICANT: ACHEN, Marc
APPLICANT: STACKER, Steven
APPLICANT: STACKER, Steven
APPLICANT: CENDRON, Angela
TITLE OF INVENTION: VBGF-C/VBGF-C/VBGF PEPTIDOMIMETIC INHIBITOR
FILE REFERENCE: 1064/48505 Achen et al
CURRENT APPLICATION NUMBER: US/09/761,636A
CURRENT FILING DATE: 2000-01-18
PRIOR APPLICATION NUMBER: US 60/176,293
PRIOR PLILNG DATE: 2000-01-18
PRIOR PLILNG DATE: 2000-01-16
PRIOR FILING DATE: 2000-05-16
NUMBER OF SEQ ID NOS: 34
SOFTWARE: Patentin version 3.0
SEQ ID NO 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
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US-10-437-963-159284
US-10-437-963-176796
US-10-437-963-187630
US-10-369-493-22558
US-10-424-599-255153
US-10-114-893-131
US-10-424-599-255153
US-10-424-599-255406
US-10-424-599-162402
US-10-424-599-162402
US-10-425-114-4313
US-10-425-114-4313
US-10-425-114-43103
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US-10-145-127-110
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; Patent No. US20020065218A1
; GENERAL INFORMATION:
              TYPE: PRT
ORGANISM: Homo sapiens
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Gaps

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APPLICANT: Boukharov, Andrey A. APPLICANT: Barbazuk, Brad APPLICANT: Barbazuk, Brad TITLE OF INVENTION: Li, Ping TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: ACHEM, MAIC
APPLICANT: ACHEM, MAIC
APPLICANT: STACKER, Steven
APPLICANT: GYACKER, Steven
APPLICANT: GYACKER, Steven
APPLICANT: GYACKER, Richard
APPLICANT: CENDRON, Angela
TITLE OF INVENTION: VEGF-D/VEGF PEPTIDOMIMETIC INHIBITOR
FILE REFERENCE: 1064/48505 Achen et al
CURRENT APPLICATION NUMBER: US/09/761,636A
CURRENT APPLICATION NUMBER: US 60/176,293
PRIOR APPLICATION NUMBER: US 60/176,293
PRIOR PLING DATE: 2000-01-18
PRIOR PLING DATE: 2000-05-16
PRIOR FILING DATE: 2000-05-16
SPRIOR FILING DATE: 2000-05-16
SOFTWARE: Patentin version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5;
TITLE OF INVENTION: VEGF-D/VEGF-C/VEGF PEPTIDOMIMETIC INHIBITOR FILE REFERENCE: 1064/48505 Achen et al CURRENT APPLICATION NUMBER: US/09/761,636A CURRENT FILING DATE: 2001-01-18 PRIOR APPLICATION NUMBER: US 60/176,293 PRIOR APPLICATION NUMBER: US 60/204,590 PRIOR APPLICATION NUMBER: US 60/204,590 PRIOR APPLICATION NUMBER: US 60/204,590 PRIOR APPLICATION NUMBER: US 60/204,590 PRIOR APPLICATION NUMBER: US 60/204,590 PRIOR ETLING DATE: 2000-05-16 NUMBER OF SEQ ID NOS: 34 SEQ ID NO. 26 SEQ ID NO. 26 SEQ ID NO. 26 SEQ ID NO. 26 SEQ ID NO. 26 SEQ ID NO. 26 SEQ ID NO. 26 SEQ ID NO. 26 SEQ ID NO. 26 SEQ ID NO. 26 SEQ ID NO. 26 SEQ ID NO. 26 SEQ ID NO. 26 SEQ ID NO. 26 SEQ ID NO. 26 SEQ ID NO. 26 SEQ ID NO. 26 SEQ ID NO. 26 SEQ ID NO. 26 SEQ ID NO. 26 SEQ ID NO. 26 SEQ ID NO. 26 SEQ ID NO. 26 SEQ ID NO. 26 SEQ ID NO. 26 SEQ ID NO. 26 SEQ ID NO. 26 SEQ ID NO. 26 SEQ ID NO. 26 SEQ ID NO. 26 SEQ ID NO. 26 SEQ ID NO. 26 SEQ ID NO. 26 SEQ ID NO. 26 SEQ ID NO. 26 SEQ ID NO. 26 SEQ ID NO. 26 SEQ ID NO. 26 SEQ ID NO. 26 SEQ ID NO. 26 SEQ ID NO. 26 SEQ ID NO. 26 SEQ ID NO. 26 SEQ ID NO. 26 SEQ ID NO. 26 SEQ ID NO. 26 SEQ ID NO. 26 SEQ ID NO. 26 SEQ ID NO. 26 SEQ ID NO. 26 SEQ ID NO. 26 SEQ ID NO. 26 SEQ ID NO. 26 SEQ ID NO. 26 SEQ ID NO. 26 SEQ ID NO. 26 SEQ ID NO. 26 SEQ ID NO. 26 SEQ ID NO. 26 SEQ ID NO. 26 SEQ ID NO. 26 SEQ ID NO. 26 SEQ ID NO. 26 SEQ ID NO. 26 SEQ ID NO. 26 SEQ ID NO. 26 SEQ ID NO. 26 SEQ ID NO. 26 SEQ ID NO. 26 SEQ ID NO. 26 SEQ ID NO. 26 SEQ ID NO. 26 SEQ ID NO. 26 SEQ ID NO. 26 SEQ ID NO. 26 SEQ ID NO. 26 SEQ ID NO. 26 SEQ ID NO. 26 SEQ ID NO. 26 SEQ ID NO. 26 SEQ ID NO. 26 SEQ ID NO. 26 SEQ ID NO. 26 SEQ ID NO. 26 SEQ ID NO. 26 SEQ ID NO. 26 SEQ ID NO. 26 SEQ ID NO. 26 SEQ ID NO. 26 SEQ ID NO. 26 SEQ ID NO. 26 SEQ ID NO. 26 SEQ ID NO. 26 SEQ ID NO. 26 SEQ ID NO. 26 SEQ ID NO. 26 SEQ ID NO. 26 SEQ ID NO. 26 SEQ ID NO. 26 SEQ ID NO. 26 SEQ ID NO. 26 SEQ ID NO. 26 SEQ ID NO. 26 SEQ ID NO. 26 SEQ ID NO. 26 SEQ ID NO. 26 SEQ ID NO. 26 SEQ ID NO. 26 SEQ ID NO. 26 SEQ ID NO. 26 SEQ ID NO. 26 SEQ ID NO. 26 SEQ I
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Pred. No. 5;
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Publication No. US20040123343A1
GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Wu, Wei
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-09-761-636A-23
; Sequence 23, Application US/09761636A
; Patent No. US20020065218A1
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Best Local Similarity 72.7%;
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                     ; TYPE: PRT
; ORGANISM: synthetic construct
US-09-761-636A-26
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Best Local Similarity
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US-10-437-963-181998
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Sequence 7, Application US/09761636A

Patent No. US20020065218A1

GENERAL INFORMATION:
APPLICANT: ACHEN, Marc

APPLICANT: STACKER, Steven

APPLICANT: ENDROW, Angela

TITLE OF INVENTION: VEGF-D/VEGF PEPTIDOMIMETIC INHIBITOR

FILE REFERENCE: 1064/48505 Achen et al

CURRENT APPLICATION NUMBER: US/09/761,636A

CURRENT FILING DATE: 2001-01-18

PRIOR APPLICATION NUMBER: US 60/176,293

PRIOR PILING DATE: 2000-01-18

PRIOR PILING DATE: 2000-01-18

PRIOR PILING DATE: 2000-01-18

NUMBER OF SEQ ID NOS: 34

NUMBER OF SEQ ID NOS: 34
                                                            APPLICANT: ACHEN, Marc
APPLICANT: ACHEN, Marc
APPLICANT: ACHEN, Marc
APPLICANT: HUGHEN, Richard
APPLICANT: HUGHEN, Richard
APPLICANT: CENDRON, Angela
TITLE OF INVENTION: VEGF-D/VEGF-C/VEGF PEPTIDOMIMETIC INHIBITOR
FILE REFERENCE: 1064/48505 Achen et al
FILE REFERENCE: 1064/48505 Achen et al
CURRENT APPLICATION NUMBER: US/09/761,636A
CURRENT FILING DATE: 2001-01-18
PRIOR APPLICATION NUMBER: US 60/176,293
PRIOR APPLICATION NUMBER: US 60/204,590
PRIOR APPLICATION NUMBER: US 60/204,590
NUMBER OF SEQ ID NOS: 34
SEQ ID NO 13
LENGTH: 10
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Pred. No. 2.6;
0; Mismatches 0; Indels
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Best Local Similarity 81.8%; Pred. No. 3.4;
Matches 9; Conservative 0; Mismatches (
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US-09-761-636A-26
; Sequence 26, Application US/09761636A
; Patent No. US20020065218A1
; GENERAL INFORMATION:
; APPLICANT: ACHEN, Marc
; APPLICANT: STACKER, Steven
; APPLICANT: HUGHES, Richard
; APPLICANT: CENDRON, Angela
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         79.8%;
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Best Local Similarity 90.0.
Best Local 9; Conservative
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                                      GENERAL INFORMATION:
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US-09-761-636A-7
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TYPE: PRT
ORGANISM: Glycine max
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Matches 5; Conserv
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US-10-424-599-258586
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NAME/KEY: unsure
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TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement FILE REPERBYCE: 38-21(53221)B
CURRENT APPLICATION NUMBER: US/10/437,963
CURRENT FILING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
LENGTH: 71
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Publication No. US20030236392A1

GENERAL INFORMATION:

APPLICANT: HELIX RESERRCH INSTITUTE

TITLE OF INVENTION: No. US20030236392A1e1 full length cDNA

FILE REFERENCE: H1-AQ105

CURRENT APPLICATION NUMBER: US/10/104,047

CURRENT APPLICATION NUMBER: 2002-03-25

PRIOR FILING DATE: 2002-03-25

NUMBER OF SEQ ID NOS: 4096

SOSTWARE: PATENTIN Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        73.1%; Score 38; DB 15; Length 208; 66.7%; Pred. No. 1.7e+02; Live 1; Mismatches 2; Indels
                                                                                                                                                                                                                                                       Score 39; DB 16; Length 71; Pred. No. 42; 3; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 119, Application US/10087192
Publication No. US20020182586A1
GENERAL INFORMATION:
APPLICANT: Mortis, David W.
APPLICANT: Engelhard, Eric K.
TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR TITLE OF INVENTION: CANCER.
FILE REPRENCE: 529452000122
CURRENT FILING DATE: 2002-03-01
PRIOR PILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: US 09/747,377
PRIOR APPLICATION NUMBER: US 09/747,377
PRIOR FILING DATE: 2000-103-02
NUMBER OF SEQ ID NOS: 2009-03-03
SOFTWARRE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                             ; OTHER INFORMATION: Clone ID: PAT_MRT4530_79226C.1.pep
US-10-437-963-181998
                                                                                                                                                                                                                                                     75.0%;
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Matches 5, Conservative
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                                                                                                                                       TYPE: PRT
ORGANISM: Oryza sativa
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ORGANISM: Homo sapiens
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ORGANISM: Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       33 CASLPLSPC 41
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57 CLSIPLIP 64
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Best Local Similarity
Matches 6; Conserv
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US-10-104-047-2520
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LENGTH: 208
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APPLICANT: La Rosa Thomas J
APPLICANT: La Rosa Thomas J
APPLICANT: Exovalic David K
APPLICANT: About Sthua
APPLICANT: About Sthua
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53223)B
CURRENT APPLICANION NUMBER: US/10/424,599
NUMBER OF SEQ ID NOS: 285684
LENGTH: 87
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Publication No. US20040031072A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: La Rosa Thomas J
APPLICANT: La Rosa Thomas J
APPLICANT: Canous Thomas J
APPLICANT: Canous J
APPLICANTION: Plants and Uses Thereof for Plant Improvement
TILLE REPERENCE: 38-21(5323)8
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 165772
LENGTH: 94
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66.7%; Pred. No. 3.2e+02;
tive 0; Mismatches 3; Indels
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55.6%; Pred. No. 1.1e+02;
tive 2; Mismatches 2; Indels
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OTHER INFORMATION: Clone ID: PAT_MRT3847_120707C.1.pep
US-10-424-599-165772
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; OTHER INFORMATION: Clone ID: PAT_MRT3847_75528C.1.pep
US-10-424-599-258586
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OTHER INFORMATION: unsure at all Xaa locations
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (1)...(413)
; OTHER INFORMATION: Xaa = Any Amino Acid
US-10-087-192-519
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 258586, Application US/10424599
Publication No. US20040031072A1
GENERAL INFORMATION:
                                                                                                                                  Query Match
Best Local Similarity 66.7°
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APPLICANT: Li, Ping
TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53221)B
CURRENT APPLICATION NUMBER: US/10/437,963
CURRENT FILING DATE: 2003-05-14
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APPLICANT: ACHEN, Marc
APPLICANT: ACHEN, Marc
APPLICANT: STACKEN, Steven
APPLICANT: CENDRON, Angela
TITLE OF INVENTION: VEGF-D/VEGF PEPTIDOMIMETIC INHIBITOR
FILE REFERENCE: 1064/48505 Achen et al
CURRENT APPLICATION NUMBER: US/09/761,636A
PRIOR APPLICATION NUMBER: US 60/76,293
PRIOR APPLICATION NUMBER: US 60/204,590
PRIOR PILING DATE: 2000-01-18
PRIOR PLING DATE: 2000-01-18
PRIOR PELING DATE: 2000-05-16
SPIOR FILING DATE: 2000-05-16
SPIOR FILING SATE: 2000-05-16
SPIOR FILING SATE: 2000-05-16
SOFTWARE: PATENTIN VOIS: 34
SOFTWARE: PATENTIN VOIS: 34
SOFTWARE: PATENTIN VOIS: 30
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PRIOR APPLICATION NUMBER: 60/350,435
PRIOR PILING DATE: 2002-01-24
PRIOR APPLICATION NUMBER: JP 2001-328381
PRIOR FILING DATE: 2001-09-14
NUMBER OF SEQ ID NOS: 3381
SOFTWARE: Patentin Ver: 2.1
SEQ ID NO 3057
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    . Sequence 25, Application US/09761636A ; Patent No. US20020065218A1
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APPLICANT: Kovalic, David K.
APPLICANT: Kovalic, David K.
APPLICANT: Cao, Yongwei
APPLICANT: Wu, Wei
APPLICANT: Bulkharov, Andrey A.
APPLICANT: Barbazuk, Brad
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             , OKGANISM: Synthetic construct
US-09-761-636A-25
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Best Local Similarity 63.6
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Best Local Similarity 55.0
Thes 5; Conservative
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202 CLSLPQAPC 210
                                                                                                                                                                                                                                                                         TYPE: PRT
ORGANISM: Homo sapiens
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US-10-437-963-148570
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Sequence 158427, Application US/10424599

Publication No. US20040031072A1

GENREAL INFORMATION:

APPLICANT: La Rosa Thomas J

APPLICANT: Cao Yongwei

APPLICANT: Cao Yongwei

TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With

TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

FILE REFERENCE: 38-21 (53223)

CURRENT APPLICATION NUMBER: US/10/424,599

CURRENT FILING DATE: 2003-04-28

NUMBER OF SEQ ID NOS: 285684

SEQ ID NO 158427

LENGTH: 149
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                                                Score 37; DB 12; Length 94; Pred. No. 1.1e+02; I Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; OTHER INFORMATION: Clone ID: PAT_MRT3847_114078C.1.pep
US-10-424-599-158427
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OTHER INFORMATION: unsure at all Xaa locations
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Sequence 3057, Application US/10094749

Publication No. US20030219741A1

GENERAL INFORMATION:
APPLICANT: SUGIYAMA, TOMOYASU
APPLICANT: OTSUKI, TETSUJI
APPLICANT: SATO, HIROYUKI
APPLICANT: SATO, HIROYUKI
APPLICANT: ISHII, SHIZUKO
APPLICANT: ISHIN, SHIZUKO
APPLICANT: ISONO, YUNO
APPLICANT: HIO, YURI
APPLICANT: HIE, RYOTARO
APPLICANT: OSSHIKA, ICHIRO
APPLICANT: TRIE, RYOTARO
APPLICANT: TRIE, RYOTARO
APPLICANT: TOSHIKAMA, TSUTOMU
APPLICANT: TOSHIKAMA, TSUTOMU
APPLICANT: MAGHIKO
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                                                          71.2%;
66.7%;
                                Query Match
Best Local Similarity 66.77
Then 6; Conservative
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Best Local Similarity 66.7
Matches 6; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT ORGANISM: Glycine max
                                                                                                                                                                                     1 CISVPLVPC 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FEATURE: NAME/KEY: unsure
                                                                                                                                                                                                                                                                                                                                             RESULT 11
US-10-424-599-158427
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US-10-094-749-3057
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RESULT 15
10-424-599-279501
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CTHER INFORMATION: Clone ID: PAT_MRT4530_48989C.l.pep

US-10-437-963-148570
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OTHER INFORMATION: Clone ID: PAT_MRT3847_94411C.1.pep
US-10-424-599-279501
NUMBER OF SEQ ID NOS: 204966
SEQ ID NO 148570
LENGTH: 53
TYPE: PRT
ORGANISM: Oryza sativa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            |:|| ::||
13 CLSVLVIPC 21
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ORGANISM: Glycine max
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Search completed: September 5, 2004, 10:29:24 Job time : 26.2727 secs

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RESULT 2
US-09-341-461-10
; Sequence 10, Application US/09341461
Sequence 5, Appli
Sequence 10, Appl
Sequence 6901, Ap
Sequence 2, Appli
Sequence 13375, A
Sequence 13375, A
Sequence 13375, A
Sequence 37, Appl
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Sequence 28, Appl
Sequence 169, App
Sequence 167, App
Sequence 7288, Ap
Sequence 7288, Ap
Sequence 3, Appli
Sequence 3, Appli
Sequence 4988, Appli
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Sequence 23997, A
Sequence 11, Appl
Sequence 12, Appl
Sequence 28, Appl
Sequence 12, Appl
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26531, A
19, Appl
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                                                                    September 5, 2004, 09:55:30; Search time 8 Seconds (without alignments) 58.079 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 1
Sequence 4
Sequence 2
Sequence 1
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/cgn2_6/ptodata/2/iaa/6A_COMB.pep:*
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/cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
       GenCore version 5.1.6
(c) 1993 - 2004 Compugen Ltd
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US-09-341-461-10
US-09-328-32-6901
US-09-328-32-6901
US-09-252-991A-27872
US-09-489-033A-13375
US-09-489-033A-13375
US-09-489-033A-13375
US-09-489-033A-13397
US-09-443-184-48
US-09-540-256-2315
US-09-443-184-48
US-09-552-991A-23997
US-09-461-69-12
US-08-609-049A-28
US-09-170-996-28
US-09-170-996-28
US-09-461-697-167
US-09-461-697-167
US-09-461-697-167
US-09-543-681A-7288
US-09-543-681A-7288
US-09-543-681A-7288
US-09-543-681A-7288
US-09-543-681A-7288
US-09-6217-3
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US-09-621-976-4028
US-09-252-991A-26531
US-09-544-716-19
                                                                                                                                                                                                                  Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                389414 seqs, 51625971 residues
                                                                                                                                                                                                                                                                           Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                  - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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                                                                                                                US-09-761-636A-14
52
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Maximum DB seq length: 200000000
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Match Length
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    Sequence 21, Appl
Sequence 11648, A
Sequence 25, Appl
Sequence 21, Appl
Sequence 21, Appl
Sequence 21, Appl
Sequence 2, Appli
Sequence 1, Appli
Sequence 1, Appli
Sequence 6, Appli
Sequence 6, Appli
Sequence 7, Appli
Sequence 1, Appli
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               | Sequence 5, Application US/08499215
| Patent No. 5612204
| GENERAL INFORMATION:
| APPLICANT: Saeki, Hisashi
| APPLICANT: Miura, Akira
| TITLE OF INVENTION: BIOLOGICAL DEGRADATIVE
| TITLE OF INVENTION: TREATMENT OF CHLORINE-SUBSTITUTED ETHYLENE
| TITLE OF INVENTION: TREATMENT OF CHLORINE-SUBSTITUTED ETHYLENE
| TITLE OF INVENTION: TREATMENT OF CHLORINE-SUBSTITUTED ETHYLENE
| CORRESPONDENCE ADDRESS:
| ADDRESSEE: Sughrue, Mion, Zinn, Macpeak & Seas
| STREET: 2100 Pennsylvania Avenue
| CITY: N.W. | STATE: Washington D.C.
                                                                                                                                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                              Sequence
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Pred. No. 24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTER: W.S.A.

ZIP: 20037-3202
COMPUTER READABLE FORM:
MEDIUW TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
SOFTWARE: & WordPerfect version 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/499,215
US-09-619-380-21
US-09-489-039A-11648
US-09-489-039A-11648
US-09-164-193-21
US-09-164-193-21
US-09-221-448A-21
PCT-US93-12019-2
US-09-546-043-5
US-09-546-043-6
US-09-546-043-6
US-09-546-043-6
US-09-546-043-7
US-09-546-043-7
US-09-546-043-7
US-09-546-043-7
US-09-546-043-7
US-09-248-588-13
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US-09-546-043-3
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US-08-937-067-7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP Hei-6-179689
FILING DATE: 08-UUL-1994
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 342 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 78.8%;
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Best Local Similarity 77.8
Matches 7; Conservative
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MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     75 CASVPLEPC 83
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-08-499-215-5
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GENERAL INFORMATION:
APPLICANT: MATC J. Rubenfield et al.
APPLICANT: MATC J. Rubenfield et al.
APPLICANT: MATC J. Rubenfield et al.
APPLICANT: MATC J. Rubenfield AND AND ACID SEQUENCES RELATING TO PSEUDOMONAS TILLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
TILLE DE INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
CURRENT APPLICATION NUMBER: US 0/09/252,991A
CURRENT PILLING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILLING DATE: 1998-02-18
PRIOR FILLING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 27872
LENGTH: 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; OTHER INFORMATION: amino acid sequence of rat cubilin protein US-09-341-461-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            69.2%; Score 36; DB 4; Length 455; 66.7%; Pred. No. 2e+02; ive 0; Mismatches 3; Indels
                                                                                              Score 38; DB 4; Length 3623;
Pred. No. 7.7e+02;
0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 37; DB 4; Length 168;
Pred. No. 51;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pred. No. 51;
2; Mismatches
                                                                                                                                                                                                                                                                                                                    Sequence 27872, Application US/09252991A
Patent No. 6551795
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-27872
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Klebsiella pneumoniae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       71.2%;
                                                                                                  Query Match 73.1%;
Best Local Similarity 66.7%;
Matches 6; Conservative
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nes 5; Conserv
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                                                                                                                                                                                                                                                                                                      US-09-252-991A-27872
      ORGANISM: rat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
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Sequence 6901.

Patent No. 6562958
GENERAL INFORMATION:
APPLICANT: Gary L. Breton et al.
APPLICANT: Gary L. Breton et al.
TITLE OF INVENTION: BAUNANNII FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: GTC99-03PA
CURRENT APPLICATION NUMBER: US/09/328,352
CURRENT FILING DATE: 1999-06-04
NUMBER OF SEQ ID NOS: 8252
SEQ ID NO 6901
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Fatent No. 6586399

GENERAL INFORMATION:

APPLICANT: Hammond, Timothy G.

TITLE OF INVENTION: Cubilin Protein, DNA Sequences Encoding Cubilin

TITLE OF INVENTION: and Uses Thereof

TITLE OF INVENTION: and Uses Thereof

FILE REFERENCE: D6148

CURRENT FPLIANG DATE: 200-07-20

PRIOR APPLICATION NUMBER: PCT/US99/01259

PRIOR FILING DATE: 1999-01-21

NUMBER OF EQ ID NOS: 40

SEQ ID NO 2

LENGTH: 3623
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GENERAL INFORMATION:
APPLICANT: Hammond, Timothy G.
APPLICANT: Verroust, Plerre J.
TITLE OF INVENTION: Cubilin Protein, DNA Sequences Encoding Cubilin TITLE OF INVENTION: and Uses Thereof
FILE REPERENCE: D6148
CURRENT APPLICATION NUMBER: US/09/341,461
CURRENT FILING DATE: 2000-07-20
PRIOR APPLICATION NUMBER: PCT/US99/01259
PRIOR PILING DATE: 1999-01-21
NUMBER OF SEQ ID NOS: 40
SEQ ID NO 10
                                                                                                                                                                                                                                                                                                                            ; OTHER INFORMATION: amino acid sequence of rat cubilin EGF5 repeat US-09-341-461-10
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                                                                                                                                                                                                                                                                                                                                                                                  Score 38; DB 4; Length 44;
Pred. No. 9.2;
0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; ORGANISM: Acinetobacter baumannii
US-09-328-352-6901
                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 66.7%;
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             273 CISVPLFHC 281
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US-09-328-352-6901
                                                                                                                                                                                                                                                                                       ORGANISM: rat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 4
US-09-341-461-2
                                                                                                                                                                                                                                                                       TYPE: PRT
                                                                                                                                                                                                                                                                                                              FEATURE:
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Gaps

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US-09-540-236-2315

Sequence 2315, Application US/09540236

Sequence 2315, Application US/09540236

Sequence 2315, Application US/09540236

GENERAL INFORMATION:

APPLICANT: Gary L. Breton et al.

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO MORAXELLA CATA!

TITLE OF INVENTION: POR DIAGNOSTICS AND THERAPEUTICS

FILE REFERENCE: 2709.2005-001

CURRENT APPLICATION NUMBER: US/09/540,236

CURRENT PILING DATE: 2000-04-04

NUMBER OF SEQ ID NOS: 3840

SEQ ID NO 2315

LENGTH: 96
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GENERAL INPORMATION:

APPLICANT: Marc J. Rubenfield et al.

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS TITLE OF INVENTION: NUCLEIC ACID AND THERAPEUTICS

FILE REPERENCE: 107196.136

CURRENT APPLICATION NUMBER: US/09/252,991A

PRIOR FILING DATE: 1999-02-18

PRIOR FILING DATE: 1999-02-18

PRIOR FILING DATE: 1999-02-18

PRIOR FILING DATE: 1999-02-18

PRIOR FILING DATE: 1999-07-27

NUMBER OF SEQ ID NOS: 33142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0;
APPLICANT: Sellhammer, Jeffrey J.
APPLICANT: Yue, Henry
APPLICANT: Wasiah
APPLICANT: Balaghn, Mariah
APPLICANT: Lal, Preeti
TITLE OF INVENTION: MAMMALIAN TOXICOLOGICAL RESPONSE MARKERS
FILE REFERENCE: PC-0007 US
CURRENT APPLICATION NUMBER: US/09/443,184A
CURRENT FILING DATE: 1999-11-19
NUMBER OF SEQ ID NOS: 138
SOFWARE: PERL PROGram
SEQ ID NO 48
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 1512;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      67.3%; Score 35; DB 4; Length 151
44.4%; Pred. No. 9.8e+02;
tive 3; Mismatches 2; Indels
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                                                                                                                                                                                                                                                                                                                                                                              ) OTHER INFORMATION: Incyte ID No. 6372431 2302721CD1 US-09-443-184-48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 34; DB 4
Pred. No. 89;
0; Mismatches
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Patent No. 6551795
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Best Local Similarity 44.4%;
Matches 4; Conservative
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Best Local Similarity 87.5
Matches 7; Conservative
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1301 CVQVVIIPC 1309
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CRGANISM: M.catarrhalis
US-09-540-236-2315
                                                                                                                                                                                                                                                                                             TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 CISVPLVPC 9
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                                                         Sequence 20960, Application US/09252991A

Sequence 20960, Application US/09252991A

Patent No. 6551795

GENERAL INFORMATION:
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS

TITLE OF INVENTION: ARRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

FILE REFERENCE: 107196.136

CURRENT APPLICATION NUMBER: US 60/074,788

PRIOR APPLICATION NUMBER: US 60/074,788

PRIOR APPLICATION NUMBER: US 60/094,190

PRIOR FILING DATE: 1998-02-18

PRIOR FILING DATE: 1998-07-27

NUMBER OF SEQ ID NOS: 33142

SEQ ID NO 20960

LENGTH: 90
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44.4%; Pred. No. 9.3e+02;
tive 3; Mismatches 2; Indels
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APPLICANT: Falco, S. Carl
APPLICANT: Falco, S. Carl
APPLICANT: Falco, S. Carl
APPLICANT: Schwaber, James S.
TITLE OF INVENTION: Plant Aminoacyl-tRNA Synthetase;
FILE REPERSING: BB-1193
CURRENT FILING DATE: 1999-07-20
FARLIER FILING DATE: 1999-07-20
FARLIER FILING DATE: July 21, 1998
NUMBER: OF SEQ ID NOS: 37
SOFTWARE: Microsoft Office 97
SEQ ID NO 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 35;
Pred. No.
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GENERAL INFORMATION:
APPLICANT: Cunningham, Mary Jane
APPLICANT: Zweiger, Gary
APPLICANT: Kaser, Matthew R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; Sequence 37, Application US/09357251
; Patent No. 6271441
                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Pseudomonas aeruginosa
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55.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4; Conservative
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1229 CVQVVIIPC 1237
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                                              JS-09-252-991A-20960
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-09-252-991A-20960
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US-09-443-184-48
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Query Match 65.4 Best Local Similarity 55.6 Matches 5; Conservative
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MOLECULE TYPE: protein
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GENERAL INFORMATION:
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Patent No. 5552273

GENERAL INFORMATION:

APPLICANT: CLEGIZIAT, Philippe L.

APPLICANT: ROBERT-BAUDOUY, Jeannine

APPLICANT: ROBERT-BAUDOUY, Jeannine

APPLICANT: GAPTAL, Jean-Pietre

TITLE OF INVENTION: POLYPETIDES CONTAINING SEQUENCES

TITLE OF INVENTION: CHARACTERISTIC OF PYRROLIDONE CARBOXYLYL PEPTIDASES,

TITLE OF INVENTION: POLYPETIDES CONTAINING A SEQUENCE CODING FOR SUCH

TITLE OF INVENTION: POLYPETIDES, AND THEIR USE, IN PARTICULAR FOR DIAGNOSTIC

NUMBER OF SEQUENCES: 43

CORRESPONDENCE ADDRESS:
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                                                                                                                               Length 147;
                                                                                                                             Ouery Match 65.4%; Score 34; DB 4; Length 147
Best Local Similarity 53.8%; Pred. No. 1.4e+02;
Matches 7; Conservative 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ZIP: 22320
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: DATE: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/107,684B
FILING DATE: 17-AUG-1993
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
NAME: Berridge william P.
REGISTRATION NUMBER: 30,024
REFERENCE/DOCKET NUMBER: WPB 28478
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-6400
TELEPHONE: (703) 836-5787
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 13
12.08-609-019A-12
; Sequence 12, Application US/08609049A
; Patent No. 5948664
                  LENGTH: 147
TYPE: PRT
ORGANISM: Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: OLIFF & BERRIDGE STREET: P.O. Box 19928
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 215 amino acids
                                                                                                                                                                                                                                                          105 CVSVARPAPAVPC 117
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Best Local Similarity
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                                                                                    US-09-252-991A-23997
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; SEQ ID NO 23997
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Gaps
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Sequence 28, Application US/08609049A
Sequence 28, Application US/08609049A
GENERAL INFORMATION:
APPLICANT: Williams, Lewis T.
APPLICANT: Molz, Lisa
APPLICANT: Chen, Yen-Wen
TILLE OF INVENTION:
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
APPLICANT: Williams, Lewis T.
APPLICANT: Molz, Lisa
APPLICANT: Chen, Yen-Wen
TITLE OF INVENTION: No. 5948664el PI 3-Kinase Polypeptides
CORRESPONDENCE: 32
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 34; DB 2; Length 1876;
Pred. No. 1.8e+03;
2; Mismatches 2; Indels
                                                                                                                                                                                                                                                    ZIP: 2000
ZIP: 20111-3834

ZIP: READABLE FORM:
MUDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARB: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/609,049A
FILING DATE: 29-FEB-1996
CLASSIFTCATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Dow, Karen B. REGISTRATION NUMBER: 29,684
REFERENCE/DOCKET NUMBER: 2307K-063700US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-326-2420
TELEPAN: 415-326-2420
TELEPAN: 413-326-2420
TELEPAN: 413-326-2422
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 1876 amino acids
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/609,049A
FILING DATE: 29-FEB-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: Townsend and Townsend and Crew LLP STREET: Two Embarcadero Center, 8th Floor CITY: San Francisco STATE: California COUNTRY: USA
                                                                                                                                              ADDRESSEE: Townsend and Townsend and Crew STREET: Two Embarcadero Center, 8th Floor CITY: San Prancisco STATE: California COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        65.4%; Scor.
55.6%; Pred. No. 1...
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1 0 **
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Sequence 12, Application US/09170996

Sequence 12, Application US/09170996

GENERAL INFORMATION:

APPLICANT: Williams, Lewis T.

APPLICANT: Williams, Lewis T.

APPLICANT: Williams, Lewis T.

APPLICANT: Ochory Yen-Wen

ITILE OF INVENTION: No. 6291220el PI 3-Kinase Polypeptides

NUMBER OF SEQUENCES: 32

CORRESPONDENCE ADDRESS:

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CITY: San Francisco

STATE: California

COUNTRY: USA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ZIP: 94111-3834
ZIP: 94111-3834
CMEDIUM TYEE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/170,996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE:

CLASSIFICATION: 435
PRIOR APPLICATION DATE:

APPLICATION NUMBER: 436
FILING DATE: 29-FEB-1996
ATTORNEY/AGENT INFORMATION:
NAME: Dow, KAZEGE B.
REGISTRATION NUMBER: 29,684
REFERENCE/DOCKET NUMBER: 2307K-063700US
TELEPHONE: 415-326-2402
TELEPHONE: 415-326-2422
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
                                                                       2307K-063700US
                 NAME: Dow, Karen B.
REGISTRATION NUMBER: 29,684
REFERENCE/DOCKET NUMBER: 23071
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-326-2402
INFORMATION FOR SEQ ID NO: 28:
SEQUENCE CHARACTERISTICS:
LENGTH: 1876 amino acids
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 1876 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                        TOPOLOGY: linear

MOLECULE TYPE: protein
US-08-609-049A-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear;

MOLECULE TYPE: protein
US-09-170-996-12
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GY: linear
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